STIC-Biotech/ChemLib 180630

From: Salmon, Katherine D.
Sent: Monday, February 27, 2006 9:03 AM
To: STIC-Biotech/ChemLib
Subject: SEquence Request

HI, this is a sequence search request for case 10/720424.
1. Please Search Seq ID No. 1
2. please search seq id NO. 8
3. Please search SEQ ID NO. 1 with word hits under 100
4. Please search SEQ ID No. 8 with word hits under 100

Thanks
Katherine Salmon
ART UNIT 1634
Mailbox REM2C70

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

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Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:12:24 ; Search time 1167.5 Seconds
(without alignments)
1411.957 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2524774

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
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10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	48.3	38	6	I17042	I17042 Sequence 53
	2	14	48.3	38	6	BD017550	BD017550 Short-cha
c	3	14	48.3	87	11	AY044145	AY044145 Synthetic
	4	13	44.8	17	6	AX578544	AX578544 Sequence
	5	13	44.8	17	6	AX579956	AX579956 Sequence
	6	13	44.8	17	6	AX580273	AX580273 Sequence
	7	13	44.8	21	6	A71350	A71350 Sequence 1
	8	13	44.8	21	6	CQ821559	CQ821559 Sequence
	9	13	44.8	41	6	BD181525	BD181525 Sequences
	10	13	44.8	41	6	AR575320	AR575320 Sequence
	11	13	44.8	41	6	AX474340	AX474340 Sequence
	12	13	44.8	42	6	CQ809558	CQ809558 Sequence
c	13	13	44.8	74	15	NEUMTTRMF	K00315 N.crassa mi
	14	12	41.4	17	6	AX578545	AX578545 Sequence
	15	12	41.4	17	6	AX579734	AX579734 Sequence
	16	12	41.4	18	6	CQ808544	CQ808544 Sequence
	17	12	41.4	18	6	CS125179	CS125179 Sequence
	18	12	41.4	18	6	AX378402	AX378402 Sequence
	19	12	41.4	20	6	AR313012	AR313012 Sequence
	20	12	41.4	20	6	AX230268	AX230268 Sequence
c	21	12	41.4	21	6	AR012649	AR012649 Sequence
c	22	12	41.4	21	6	AR096779	AR096779 Sequence
c	23	12	41.4	23	6	CQ799486	CQ799486 Sequence
	24	12	41.4	29	6	AX825701	AX825701 Sequence
	25	12	41.4	31	6	AX665947	AX665947 Sequence
	26	12	41.4	34	6	E04767	E04767 Synthetic D
c	27	12	41.4	41	6	AX514339	AX514339 Sequence
c	28	12	41.4	41	6	AX519906	AX519906 Sequence
	29	12	41.4	48	6	AX230265	AX230265 Sequence
	30	12	41.4	50	6	AX161514	AX161514 Sequence
	31	12	41.4	50	6	AX161516	AX161516 Sequence
	32	12	41.4	50	8	AY728744	AY728744 Macaca mu
c	33	12	41.4	51	6	AX158711	AX158711 Sequence
c	34	12	41.4	51	6	AX158712	AX158712 Sequence
c	35	12	41.4	51	6	AX158713	AX158713 Sequence
c	36	12	41.4	51	6	AX158714	AX158714 Sequence
	37	12	41.4	51	6	AX161509	AX161509 Sequence
	38	12	41.4	51	6	AX161511	AX161511 Sequence
	39	12	41.4	51	6	AX161513	AX161513 Sequence
	40	12	41.4	51	6	AX161515	AX161515 Sequence
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c	42	12	41.4	60	6	CQ541463	CQ541463 Sequence
c	43	12	41.4	60	6	CQ541937	CQ541937 Sequence
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	45	12	41.4	65	6	CQ557874	CQ557874 Sequence

ALIGNMENTS

RESULT 1
I17042
LOCUS I17042 38 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 53 from patent US 5484699.
ACCESSION I17042
VERSION I17042.1 GI:1251950
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Bouma,S.R., Joseph,J.L., Marshall,R.L. and Laffler,T.G.
TITLE Nucleotide sequences useful as type specific probes, PCR primers and LCR probes for the amplification and detection of human papilloma virus, and related kits and methods
JOURNAL Patent: US 5484699-A 53 16-JAN-1996;
FEATURES Location/Qualifiers
source 1. .38
/organism="unknown"
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ORIGIN

Query Match 48.3%; Score 14; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGT 14
||||||||||||||
Db 1 GATGGTGATATGGT 14

RESULT 2
BD017550
LOCUS BD017550 38 bp DNA linear PAT 27-AUG-2002
DEFINITION Short-chain nucleotide sequence of human papilloma virus.
ACCESSION BD017550
VERSION BD017550.1 GI:22558726
KEYWORDS JP 2001231587-A/53.
SOURCE unidentified
ORGANISM unidentified
unclassified.

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REFERENCE   1  (bases 1 to 38)
  AUTHORS   Joseph,J.L., Borma,S.R., Marshall,R.L. and Rahler,T.G.
  TITLE     Short-chain nucleotide sequence of human papilloma virus
  JOURNAL   Patent: JP 2001231587-A 53 28-AUG-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Unidentified
            PN   JP 2001231587-A/53
            PD   28-AUG-2001
            PF   31-JAN-2001 JP 2001023849
            PR   28-SEP-1990 US       589948,28-SEP-1990 US       590105 PR
            28-SEP-1990 US       590253
            PI   JEFFREY L JOSEPH,STANLEY R BORMA,RONALD L MARSHALL,THOMAS G
            PI   RAHLER
            PC   C12N15/09,C12M1/00,C12Q1/68//(C12N15/09,C12R1:93),C12N15/00,
            PC   (C12N15/00,C12R1:93)
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            CC   Topology: Linear;
            CC   Short-chain nucleotide sequence of human papilloma virus FH
            Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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ORIGIN

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Qy          1 GATGGTGATATGGT 14
              ||||||||||||||
Db          1 GATGGTGATATGGT 14


RESULT 3
AY044145/c
LOCUS       AY044145                  87 bp    DNA     linear   SYN 15-SEP-2001
DEFINITION  Synthetic construct nitrogen regulatory cis element sequence.
ACCESSION   AY044145
VERSION     AY044145.1  GI:15625236
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 87)
  AUTHORS   Peng,R., Yao,Q., Xiong,A., Li,X. and Fan,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-2001) Shanghai Yong Ye Agro-Bioengineering Co.,
            Ltd, Shanghai Academy of Agricultural Sciences, Beidi Road 2901,
            Shanghai 201106, China
FEATURES              Location/Qualifiers
     source           1. .87
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
                      /note="contains five copies of the nitrogen regulatory
                      element (TATCTA); can be inserted into lacZ reporter
                      plasmid for yeast one-hybrid system"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GATATGGTAGATAC 20
              ||||||||||||||
Db         43 GATATGGTAGATAC 30


RESULT 4
AX578544
LOCUS       AX578544                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 382 from Patent WO0211674.
ACCESSION   AX578544
VERSION     AX578544.1  GI:27647746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 382 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES              Location/Qualifiers
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Qy         10 ATGGTAGATACAG 22
              |||||||||||||
Db          4 ATGGTAGATACAG 16


RESULT 5
AX579956
LOCUS       AX579956                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 1794 from Patent WO0211674.
ACCESSION   AX579956
VERSION     AX579956.1  GI:27649158
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1794 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES              Location/Qualifiers
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
              |||||||||||||
Db          2 ATGGTAGATACAG 14


RESULT 6
AX580273
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LOCUS       AX580273                 17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 2111 from Patent WO0211674.
ACCESSION   AX580273
VERSION     AX580273.1  GI:27649475
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 2111 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
               |||||||||||||
Db          3 ATGGTAGATACAG 15


RESULT 7
A71350
LOCUS       A71350                   21 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 1 from Patent WO9811253.
ACCESSION   A71350
VERSION     A71350.1  GI:4774983
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Ernest,I., Remacle,J., Alexandre,I. and Zammatteo,N.
  TITLE     METHOD AND KIT FOR DIAGNOSING AND/OR QUANTIFYING BY SANDWICH
            HYBRIDISATION OF NUCLEIC ACID SEQUENCES ON SOLID SUPPORT
  JOURNAL   Patent: WO 9811253-A 1 19-MAR-1998;
            ERNEST ISABELLE (BE)
FEATURES             Location/Qualifiers
     source          1. .21
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ORIGIN

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Qy          1 GATGGTGATATGG 13
              |||||||||||||
Db          9 GATGGTGATATGG 21


RESULT 8
CQ821559
LOCUS       CQ821559                 21 bp    DNA     linear   PAT 21-JUN-2004
DEFINITION  Sequence 67 from Patent WO2004047863.
ACCESSION   CQ821559
VERSION     CQ821559.1  GI:49019333
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Sahin,U., Tuereci,O. and Koslowski,M.
  TITLE     Genetic products differentially expressed in tumors and the use
            thereof
  JOURNAL   Patent: WO 2004047863-A 67 10-JUN-2004;
            Ganymed Pharmaceuticals AG (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         10 ATGGTAGATACAG 22
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Db          7 ATGGTAGATACAG 19


RESULT 9
BD181525
LOCUS       BD181525                 41 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Sequences and methods for detection of HIV-1.
ACCESSION   BD181525
VERSION     BD181525.1  GI:30792443
KEYWORDS    JP 2002330790-A/1.
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Hellyer,T.J., You,Q. and Harris,J.M.
  TITLE     Sequences and methods for detection of HIV-1
  JOURNAL   Patent: JP 2002330790-A 1 19-NOV-2002;
            BECTON DICKINSON AND CO
COMMENT     OS   Human immunodeficiency virus type 1
            PN   JP 2002330790-A/1
            PD   19-NOV-2002
            PF   09-JAN-2002 JP 2002002066
            PR   09-JAN-2001 US    09/757207
            PI   TOBIN J HELLYER,QIMIN YOU,JAMES M HARRIS
            PC   C12N15/09,C12Q1/68,C12N15/00
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            FT                   1'.
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ORIGIN

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Qy         12 GGTAGATACAGGA 24
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Db         23 GGTAGATACAGGA 35


RESULT 10
AR575320
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LOCUS       AR575320                41 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 1 from patent US 6770752.
ACCESSION   AR575320
VERSION     AR575320.1  GI:56576305
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Hellyer,T.J., You,Q. and Harris,J.M.
  TITLE     Sequences for detection of HIV-1
  JOURNAL   Patent: US 6770752-A 1 03-AUG-2004;
            Becton, Dickinson and Company; Franklin Lakes, NJ
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         12 GGTAGATACAGGA 24
              |||||||||||||
Db         23 GGTAGATACAGGA 35


RESULT 11
AX474340
LOCUS       AX474340                41 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1 from Patent EP1223227.
ACCESSION   AX474340
VERSION     AX474340.1  GI:22213946
KEYWORDS    .
SOURCE      Human immunodeficiency virus 1 (HIV-1)
  ORGANISM  Human immunodeficiency virus 1
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
  AUTHORS   Hellyer,T.J., You,Q. and Harris,J.M.
  TITLE     Sequences and methods for detection of hiv-1
  JOURNAL   Patent: EP 1223227-A 1 17-JUL-2002;
            Becton, Dickinson and Company (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGTAGATACAGGA 24
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Db         23 GGTAGATACAGGA 35


RESULT 12
CQ809558
LOCUS       CQ809558                42 bp    DNA     linear   PAT 10-MAY-2004
DEFINITION  Sequence 861 from Patent WO2003097790.
ACCESSION   CQ809558
VERSION     CQ809558.1  GI:47114973
KEYWORDS    .
SOURCE      Nicotiana tabacum (common tobacco)
  ORGANISM  Nicotiana tabacum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1
  AUTHORS   Inz,D.G., Goossens,A., Oksman-Caldentey,K.M., Haekkinen,S.T. and
            Laakso,I.J.
  TITLE     Genes and uses thereof to modulate secondary metabolite
            biosynthesis
  JOURNAL   Patent: WO 2003097790-A 861 27-NOV-2003;
            Vlaams Interuniversitair Instituut voor Biotechnologie vz w. (BE);
            VTT Biotechnology (FI)
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ORIGIN

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Qy          4 GGTGATATGGTAG 16
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Db         22 GGTGATATGGTAG 34


RESULT 13
NEUMTTRMF/c
LOCUS       NEUMTTRMF               74 bp    tRNA    linear   PLN 20-MAY-1994
DEFINITION  N.crassa mitochondrial initiator Met-tRNA-f.
ACCESSION   K00315
VERSION     K00315.1  GI:175545
KEYWORDS    transfer RNA; transfer RNA-Met.
SOURCE      mitochondrion Neurospora crassa
  ORGANISM  Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE   1  (bases 1 to 74)
  AUTHORS   Heckman,J.E., Hecker,L.I., Schwartzbach,S.D., Barnett,W.E.,
            Baumstark,B. and RajBhandary,U.L.
  TITLE     Structure and function of initiator methionine tRNA from the
            mitochondria of Neurospora crassa
  JOURNAL   Cell 13 (1), 83-95 (1978)
   PUBMED   145896
COMMENT     Original source text: Neurospora crassa (strain or23-ia)
            mitochondrial tRNA.
            Contributed on tape April 1983 by M.Sprinzl & D.H.Gauss; from their
            entry 1360 in Nucleic Acids Res. 11, r1-r54 (1983). N.crassa mt
            Met-tRNA-f resembles that of eukaryotic organisms in its structure,
            but its sequence homology is closer to prokaryotic sequences
            (although it resembles neither to any great extent [1]).
FEATURES             Location/Qualifiers
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ORIGIN      5' end of mature tRNA.

  Query Match            44.8%;  Score 13;  DB 15;  Length 74;
  Best Local Similarity  100.0%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 GATACAGGATTTG 28
```

```
              ||||||||||||
Db         66 GATACAGGATTTG 54


RESULT 14
AX578545
LOCUS       AX578545                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 383 from Patent WO0211674.
ACCESSION   AX578545
VERSION     AX578545.1  GI:27647747
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 383 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TGGTAGATACAG 22
              ||||||||||||
Db          1 TGGTAGATACAG 12


RESULT 15
AX579734
LOCUS       AX579734                  17 bp    RNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 1572 from Patent WO0211674.
ACCESSION   AX579734
VERSION     AX579734.1  GI:27648936
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
            and Grupe,A.
  TITLE     Method and reagent for the inhibition of calcium activated chloride
            channel-1 (clca-1)
  JOURNAL   Patent: WO 0211674-A 1572 14-FEB-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
            Thompson, James (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACA 21
              ||||||||||||
```

```
Db          6 ATGGTAGATACA 17

Search completed: March  6, 2006, 00:38:39
Job time : 1169.5 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:08:34 ; Search time 271.5 Seconds
(without alignments)
711.882 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 5288170

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	29	12	ADQ27978	Adq27978 Human pap
	2	17	58.6	24	12	ADQ27979	Adq27979 Human pap
	3	14	48.3	33	12	ADQ27982	Adq27982 Human pap
c	4	13	44.8	65	6	ABN29627	Abn29627 Rat splic
c	5	13	44.8	93	4	AAK39536	Aak39536 Human bon
c	6	13	44.8	93	4	AAK13792	Aak13792 Human bra
c	7	13	44.8	93	6	ABS13626	Abs13626 Human gen
	8	12	41.4	19	3	AAA86383	Aaa86383 PCBA HH r
	9	12	41.4	19	3	AAA86382	Aaa86382 PCBA HH r
	10	12	41.4	19	3	AAA86384	Aaa86384 PCBA HH r
	11	12	41.4	19	5	AAH61545	Aah61545 PCNA HH r
	12	12	41.4	19	5	AAH61544	Aah61544 PCNA HH r
	13	12	41.4	19	5	AAH61546	Aah61546 PCNA HH r
c	14	12	41.4	21	14	ACL53645	Acl53645 TRPM4 siR
	15	12	41.4	21	14	ACL53388	Acl53388 TRPM4 siR
	16	12	41.4	21	14	ACL53646	Acl53646 TRPM4 siR
c	17	12	41.4	21	14	ACL53644	Acl53644 TRPM4 tar
c	18	12	41.4	21	14	ACL53386	Acl53386 TRPM4 tar
c	19	12	41.4	21	14	ACL53387	Acl53387 TRPM4 siR
	20	12	41.4	23	13	ADR45742	Adr45742 Strand #3
	21	12	41.4	23	14	ADW08970	Adw08970 siRNA-dup
c	22	12	41.4	50	14	ADY22209	Ady22209 Murine fu
c	23	12	41.4	50	14	ADY22200	Ady22200 Murine fu
c	24	12	41.4	60	6	ABN36247	Abn36247 Human spl
	25	12	41.4	65	6	ABN52768	Abn52768 Mouse spl
c	26	12	41.4	65	6	ABN54463	Abn54463 Mouse spl
	27	12	41.4	65	6	ABN29150	Abn29150 Rat splic
c	28	12	41.4	68	13	ADR91004	Adr91004 DNA enzym
	29	11	37.9	11	6	ABV68952	Abv68952 Human ski
	30	11	37.9	11	12	ADQ34847	Adq34847 Human fac
c	31	11	37.9	15	6	ABL45752	Abl45752 Human MMP
c	32	11	37.9	17	4	AAF99546	Aaf99546 Immunosti
c	33	11	37.9	17	6	ABS78262	Abs78262 Angiogene
c	34	11	37.9	17	6	ABL39094	Abl39094 Immunosti
	35	11	37.9	17	8	ABT37250	Abt37250 Tumour su
c	36	11	37.9	17	9	ACH03084	Ach03084 Immunosti
c	37	11	37.9	17	9	ADB37048	Adb37048 Immunosti
	38	11	37.9	17	10	ADB41706	Adb41706 Tumour su
	39	11	37.9	17	10	ADB39774	Adb39774 Tumour su
	40	11	37.9	17	10	ADB43518	Adb43518 Tumour su
	41	11	37.9	17	10	ACC52664	Acc52664 Human tum
c	42	11	37.9	17	13	ADU90062	Adu90062 Allergic
	43	11	37.9	18	2	AAQ37432	Aaq37432 Probe B1-
c	44	11	37.9	18	4	AAH44097	Aah44097 Oryza sat
	45	11	37.9	18	11	ADM06615	Adm06615 Human PCR

ALIGNMENTS

RESULT 1
ADQ27978
ID ADQ27978 standard; DNA; 29 BP.
XX
AC ADQ27978;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human papillomavirus genotype detection PCR primer #8.
XX
KW ss; primer; detection; diagnosis; amplification;
KW Human Papillomavirus genotype; cervical-neoplasia;
KW oncogenic high-risk group.
XX
OS Human papillomavirus.
XX
PN WO2004050917-A1.
XX
PD 17-JUN-2004.
XX
PF 28-NOV-2003; 2003WO-KR002608.
XX
PR 29-NOV-2002; 2002KR-00075370.
PR 31-JUL-2003; 2003KR-00053147.
XX
PA (ALBI-) ALBIOMED CO LTD.
XX
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;
XX
DR WPI; 2004-450746/42.
XX
PT New general primer or primer pair, useful for amplifying and detecting,
PT or for use in a nucleic acid amplification process for amplifying Human
PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT genotypes.
XX
PS Claim 2; SEQ ID NO 8; 71pp; English.
XX
CC The invention relates to a general primer or primer pair for amplifying
CC and detecting or for use in a nucleic acid amplification process for
CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC useful for amplifying cervical-neoplasia related HPV genotypes including

```
CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 29 BP; 8 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 12;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-07;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              |||||||||||||||||||||||||||||
Db          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29


RESULT 2
ADQ27979
ID   ADQ27979 standard; DNA; 24 BP.
XX
AC   ADQ27979;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human papillomavirus genotype detection PCR primer #9.
XX
KW   ss; primer; detection; diagnosis; amplification;
KW   Human Papillomavirus genotype; cervical-neoplasia;
KW   oncogenic high-risk group.
XX
OS   Human papillomavirus.
XX
PN   WO2004050917-A1.
XX
PD   17-JUN-2004.
XX
PF   28-NOV-2003; 2003WO-KR002608.
XX
PR   29-NOV-2002; 2002KR-00075370.
PR   31-JUL-2003; 2003KR-00053147.
XX
PA   (ALBI-) ALBIOMED CO LTD.
XX
PI   Lee S,  Kim Y,  Yu K,  Kim S,  Cha K,  Ko J;
XX
DR   WPI; 2004-450746/42.
XX
PT   New general primer or primer pair, useful for amplifying and detecting,
PT   or for use in a nucleic acid amplification process for amplifying Human
PT   Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT   genotypes.
XX
PS   Claim 2; SEQ ID NO 9; 71pp; English.
XX
CC   The invention relates to a general primer or primer pair for amplifying
CC   and detecting or for use in a nucleic acid amplification process for
CC   amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC   useful for amplifying cervical-neoplasia related HPV genotypes including
CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 24 BP; 10 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             58.6%;  Score 17;  DB 12;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.1;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ACCATAGAGCCACTAGG 29
              |||||||||||||||||
Db          8 ACCATAGAGCCACTAGG 24


RESULT 3
ADQ27982
ID   ADQ27982 standard; DNA; 33 BP.
XX
AC   ADQ27982;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human papillomavirus genotype detection PCR primer #12.
XX
KW   ss; primer; detection; diagnosis; amplification;
KW   Human Papillomavirus genotype; cervical-neoplasia;
KW   oncogenic high-risk group.
XX
OS   Human papillomavirus.
XX
PN   WO2004050917-A1.
XX
PD   17-JUN-2004.
XX
PF   28-NOV-2003; 2003WO-KR002608.
XX
PR   29-NOV-2002; 2002KR-00075370.
PR   31-JUL-2003; 2003KR-00053147.
XX
PA   (ALBI-) ALBIOMED CO LTD.
XX
PI   Lee S,  Kim Y,  Yu K,  Kim S,  Cha K,  Ko J;
XX
DR   WPI; 2004-450746/42.
XX
PT   New general primer or primer pair, useful for amplifying and detecting,
PT   or for use in a nucleic acid amplification process for amplifying Human
PT   Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT   genotypes.
XX
PS   Claim 2; SEQ ID NO 12; 71pp; English.
XX
CC   The invention relates to a general primer or primer pair for amplifying
CC   and detecting or for use in a nucleic acid amplification process for
CC   amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC   useful for amplifying cervical-neoplasia related HPV genotypes including
CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 33 BP; 13 A; 6 C; 7 G; 7 T; 0 U; 0 Other;

  Query Match             48.3%;  Score 14;  DB 12;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ACCATAGAGCCACT 26
              ||||||||||||||
Db         20 ACCATAGAGCCACT 33


RESULT 4
ABN29627/c
ID   ABN29627 standard; DNA; 65 BP.
XX
AC   ABN29627;
XX
DT   15-JUL-2002  (first entry)
XX
```

DE Rat spliced transcript detection oligonucleotide SEQ ID NO:2375.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Rattus norvegicus.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 2375; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 65 BP; 17 A; 11 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ACCATAGAGCCAC 25
||||||||||||
Db 34 ACCATAGAGCCAC 22

RESULT 5
AAK39536/c
ID AAK39536 standard; DNA; 93 BP.
XX
AC AAK39536;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed single exon probe SEQ ID NO: 14093.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 14093; 658pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow
CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
CC the probes of the invention
XX
SQ Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATAGAGCCACTAG 28
||||||||||||
Db 58 ATAGAGCCACTAG 46

RESULT 6
AAK13792/c
ID AAK13792 standard; DNA; 93 BP.
XX
AC AAK13792;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe SEQ ID NO: 13783.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 13783; 650pp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATAGAGCCACTAG 28
||||||||||||||
Db 58 ATAGAGCCACTAG 46

RESULT 7
ABS13626/c
ID ABS13626 standard; DNA; 93 BP.
XX
AC ABS13626;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 13617.
XX
KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesis; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2002-114183/15.
XX
PT Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 4; SEQ ID NO 13617; 634pp; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesis, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 93 BP; 29 A; 27 C; 15 G; 22 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATAGAGCCACTAG 28
||||||||||||||
Db 58 ATAGAGCCACTAG 46

RESULT 8
AAA86383
ID AAA86383 standard; DNA; 19 BP.
XX
AC AAA86383;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCBA HH ribozyme binding site #115.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.

XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 107; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTACCATAGAG 21
||||||||||||
Db 7 GTTACCATAGAG 18

RESULT 9
AAA86382
ID AAA86382 standard; DNA; 19 BP.
XX
AC AAA86382;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCBA HH ribozyme binding site #114.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 107; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTACCATAGAG 21
||||||||||||
Db 8 GTTACCATAGAG 19

RESULT 10
AAA86384
ID AAA86384 standard; DNA; 19 BP.
XX
AC AAA86384;
XX
DT 04-DEC-2000 (first entry)
XX
DE PCBA HH ribozyme binding site #116.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 107; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 7 A; 2 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTACCATAGAG 21
||||||||||||

```
Db          2 GTTACCATAGAG 13


RESULT 11
AAH61545
ID   AAH61545 standard; DNA; 19 BP.
XX
AC   AAH61545;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:3969.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 360; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 7 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             41.4%;  Score 12;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 GTTACCATAGAG 21
               ||||||||||||
Db           7 GTTACCATAGAG 18


RESULT 12
AAH61544
ID   AAH61544 standard; DNA; 19 BP.
XX
AC   AAH61544;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:3968.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;   99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 360; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             41.4%;  Score 12;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
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  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          8 GTTACCATAGAG 19


RESULT 13
AAH61546
ID   AAH61546 standard; DNA; 19 BP.
XX
AC   AAH61546;
XX
DT   10-SEP-2001  (first entry)
XX
DE   PCNA HH ribozyme binding site SEQ ID NO:3970.
XX
KW   Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW   recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW   proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW   cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW   matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW   antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW   antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW   atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW   basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW   sickle cell retinopathy; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200130362-A2.
XX
PD   03-MAY-2001.
XX
PF   26-OCT-2000; 2000WO-US029500.
XX
PR   26-OCT-1999;  99US-0161532P.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Robbins JM,  Tritz R;
XX
DR   WPI; 2001-300427/31.
XX
PT   Treating proliferative skin or eye diseases and scarring, using ribozymes
PT   that cleave RNA encoding cytokines involved in inflammation, matrix
PT   metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS   Example 1; Page 360; 408pp; English.
XX
CC   The present invention describes a method for treating a proliferative
CC   skin or eye disease and scarring. The method involves administering a
CC   ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC   inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC   dependent kinase, growth factor or a reductase, or administering a
CC   nucleic acid molecule (II) comprising a promoter operably linked to a
CC   nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC   dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC   ophthalmological, vulnerary, keratolytic and virucide activities, and
CC   cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC   in gene therapy. (I) and (II) are useful for treating proliferative skin
CC   diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC   squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC   also be used for treating proliferative eye diseases such as diabetic
CC   retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC   prematurity and retinal detachment, and for treating and preventing
CC   scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC   scar. AAH57577 to AAH62099 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 19 BP; 7 A; 2 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match            41.4%;  Score 12;  DB 5;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 2.9e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          2 GTTACCATAGAG 13


RESULT 14
ACL53645/c
ID   ACL53645 standard; RNA; 21 BP.
XX
AC   ACL53645;
XX
DT   24-MAR-2005  (first entry)
XX
DE   TRPM4 siRNA sense sequence, SEQ ID 14717.
XX
KW   Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW   short interfering RNA; gene silencing.
XX
OS   Synthetic.
XX
PN   WO2005001092-A2.
XX
PD   06-JAN-2005.
XX
PF   19-MAY-2004; 2004WO-US015645.
XX
PR   20-MAY-2003; 2003US-0471729P.
XX
PA   (AMHP ) WYETH.
XX
PI   Be X,  Wei L,  Slonim DK,  Howes SH;
XX
DR   WPI; 2005-075568/08.
XX
PT   Pharmaceutical composition comprising an agent capable of modulating an
PT   expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT   activated by the polypeptide or antibody, and a carrier, useful for
PT   treating cancer.
XX
PS   Claim 3; SEQ ID NO 14717; 113pp; English.
XX
CC   The present invention relates to a novel pharmaceutical composition
CC   comprising: (a) an agent capable of modulating an expression level or
CC   protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC   ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC   (b) a carrier. The pharmaceutical composition may also comprise a
CC   polynucleotide capable of inhibiting or decreasing the expression of the
CC   CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC   invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC   FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC   pharmaceutical composition is useful for treating cancer, e.g. colon
CC   cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC   cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC   CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 21 BP; 2 A; 8 C; 4 G; 0 T; 7 U; 0 Other;

  Query Match            41.4%;  Score 12;  DB 14;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 2.9e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         18 AGAGCCACTAGG 29
              ||||||||||||
Db         12 AGAGCCACTAGG 1
```

RESULT 15
ACL53388
ID ACL53388 standard; RNA; 21 BP.
XX
AC ACL53388;
XX
DT 24-MAR-2005 (first entry)
XX
DE TRPM4 siRNA antisense sequence, SEQ ID 14460.
XX
KW Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
OS Synthetic.
XX
PN WO2005001092-A2.
XX
PD 06-JAN-2005.
XX
PF 19-MAY-2004; 2004WO-US015645.
XX
PR 20-MAY-2003; 2003US-0471729P.
XX
PA (AMHP) WYETH.
XX
PI Be X, Wei L, Slonim DK, Howes SH;
XX
DR WPI; 2005-075568/08.
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
PS Claim 3; SEQ ID NO 14460; 113pp; English.
XX
CC The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 5 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 41.4%; Score 12; DB 14; Length 21;
Best Local Similarity 91.7%; Pred. No. 2.9e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         18 AGAGCCACTAGG 29
               ||||||||:|||
Db          2 AGAGCCACUAGG 13
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	15	51.7	25	7	US-10-719-956-390726	Sequence 390726,
	4	14	48.3	33	8	US-10-720-424B-12	Sequence 12, Appl
	5	14	48.3	98	3	US-09-969-373-1120	Sequence 1120, Ap
c	6	13	44.8	25	7	US-10-719-956-48748	Sequence 48748, A
	7	13	44.8	25	7	US-10-719-956-77937	Sequence 77937, A
	8	13	44.8	25	7	US-10-719-956-100361	Sequence 100361,
c	9	13	44.8	25	7	US-10-719-956-587629	Sequence 587629,
	10	13	44.8	25	7	US-10-719-956-590305	Sequence 590305,
c	11	13	44.8	25	8	US-10-719-900-203048	Sequence 203048,
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	13	13	44.8	25	8	US-10-719-900-403733	Sequence 403733,
	14	13	44.8	25	8	US-10-719-900-968422	Sequence 968422,
c	15	13	44.8	25	9	US-10-843-527-84223	Sequence 84223, A
	16	13	44.8	25	9	US-10-843-527-153954	Sequence 153954,
	17	13	44.8	25	10	US-11-036-317-11970	Sequence 11970, A
	18	13	44.8	25	10	US-11-036-317-37797	Sequence 37797, A
	19	13	44.8	25	10	US-11-036-317-48131	Sequence 48131, A
	20	13	44.8	25	10	US-11-036-317-112161	Sequence 112161,
c	21	13	44.8	25	10	US-11-036-317-760555	Sequence 760555,
	22	13	44.8	25	10	US-11-036-317-868243	Sequence 868243,
	23	13	44.8	25	10	US-11-036-317-870363	Sequence 870363,
c	24	13	44.8	65	3	US-09-908-975-2375	Sequence 2375, Ap
c	25	13	44.8	93	3	US-09-864-761-26662	Sequence 26662, A
	26	12	41.4	21	8	US-10-751-736-37321	Sequence 37321, A
	27	12	41.4	21	8	US-10-751-736-37322	Sequence 37322, A
	28	12	41.4	21	8	US-10-751-736-37591	Sequence 37591, A
	29	12	41.4	21	8	US-10-751-736-37592	Sequence 37592, A
	30	12	41.4	21	8	US-10-751-736-37594	Sequence 37594, A
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c	33	12	41.4	21	9	US-10-847-918-14459	Sequence 14459, A
	34	12	41.4	21	9	US-10-847-918-14460	Sequence 14460, A
c	35	12	41.4	21	9	US-10-847-918-14716	Sequence 14716, A
c	36	12	41.4	21	9	US-10-847-918-14717	Sequence 14717, A
	37	12	41.4	21	9	US-10-847-918-14718	Sequence 14718, A
c	38	12	41.4	25	7	US-10-719-956-25244	Sequence 25244, A
	39	12	41.4	25	7	US-10-719-956-235258	Sequence 235258,
c	40	12	41.4	25	7	US-10-719-956-356087	Sequence 356087,
	41	12	41.4	25	7	US-10-719-956-374911	Sequence 374911,
	42	12	41.4	25	7	US-10-719-956-406488	Sequence 406488,
c	43	12	41.4	25	7	US-10-719-956-468308	Sequence 468308,
c	44	12	41.4	25	7	US-10-719-956-468309	Sequence 468309,
	45	12	41.4	25	7	US-10-719-956-484683	Sequence 484683,

ALIGNMENTS

RESULT 1
US-10-720-424B-8
; Sequence 8, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-8

Query Match 100.0%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
||||||||||||||||||||||||||||||
Db 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29

RESULT 2
US-10-720-424B-9
; Sequence 9, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo

; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-9

Query Match 58.6%; Score 17; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ACCATAGAGCCACTAGG 29
|||||||||||||||||
Db 8 ACCATAGAGCCACTAGG 24

RESULT 3
US-10-719-956-390726/c
; Sequence 390726, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 390726
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-390726

Query Match 51.7%; Score 15; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CATAGAGCCACTAGG 29
|||||||||||||||
Db 19 CATAGAGCCACTAGG 5

RESULT 4
US-10-720-424B-12
; Sequence 12, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-12

Query Match 48.3%; Score 14; DB 8; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ACCATAGAGCCACT 26
||||||||||||||
Db 20 ACCATAGAGCCACT 33

RESULT 5
US-09-969-373-1120
; Sequence 1120, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1120
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1120

Query Match 48.3%; Score 14; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTACCATAGAGCCA 24
||||||||||||||
Db 63 TTACCATAGAGCCA 76

RESULT 6
US-10-719-956-48748/c
; Sequence 48748, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48748
; LENGTH: 25

```
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-48748

  Query Match             44.8%;  Score 13;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACC 15
              |||||||||||||
Db         15 GTCAGAGGTTACC 3


RESULT 7
US-10-719-956-77937
; Sequence 77937, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77937
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-77937

  Query Match             44.8%;  Score 13;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACC 15
              |||||||||||||
Db          9 GTCAGAGGTTACC 21


RESULT 8
US-10-719-956-100361
; Sequence 100361, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 100361
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-100361

  Query Match             44.8%;  Score 13;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 CCATAGAGCCACT 26
              |||||||||||||
Db         11 CCATAGAGCCACT 23


RESULT 9
US-10-719-956-587629/c
; Sequence 587629, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 587629
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-587629

  Query Match             44.8%;  Score 13;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCA 16
              |||||||||||||
Db         20 TCAGAGGTTACCA 8


RESULT 10
US-10-719-956-590305
; Sequence 590305, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
;  CURRENT APPLICATION NUMBER: US/10/719,956
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,836
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 699466
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 590305
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-719-956-590305

  Query Match             44.8%;  Score 13;  DB 7;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ACCATAGAGCCAC 25
              |||||||||||||
Db          9 ACCATAGAGCCAC 21


RESULT 11
US-10-719-900-203048/c
; Sequence 203048, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 203048
;   LENGTH: 25
;   TYPE: DNA
```

; ORGANISM: Mus musculus
US-10-719-900-203048

Query Match 44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGAGGTTACCAT 17
||||||||||||
Db 22 CAGAGGTTACCAT 10

RESULT 12
US-10-719-900-295168/c
; Sequence 295168, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 295168
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-295168

Query Match 44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CCATAGAGCCACT 26
||||||||||||
Db 17 CCATAGAGCCACT 5

RESULT 13
US-10-719-900-403733
; Sequence 403733, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 403733
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-403733

Query Match 44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CATAGAGCCACTA 27
||||||||||||
Db 12 CATAGAGCCACTA 24

RESULT 14
US-10-719-900-968422
; Sequence 968422, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 968422
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-968422

Query Match 44.8%; Score 13; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CATAGAGCCACTA 27
||||||||||||
Db 12 CATAGAGCCACTA 24

RESULT 15
US-10-843-527-84223/c
; Sequence 84223, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 84223
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-84223

Query Match 44.8%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGTCAGAGGTTA 13
||||||||||||
Db 14 GCGTCAGAGGTTA 2

Search completed: March 5, 2006, 23:01:35
Job time : 361 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:22:58 ; Search time 449.5 Seconds
(without alignments)
141.451 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7218535 seqs, 1096242582 residues

Word size: 1

Total number of hits satisfying chosen parameters: 11882884

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	44.8	19	10	US-11-101-244-1039686	Sequence 1039686,
2	13	44.8	19	11	US-11-083-784-1039686	Sequence 1039686,
3	13	44.8	25	12	US-11-121-849-210096	Sequence 210096,
c 4	13	44.8	25	12	US-11-121-849-235837	Sequence 235837,
c 5	13	44.8	25	12	US-11-121-849-417792	Sequence 417792,
6	13	44.8	25	12	US-11-136-527-105826	Sequence 105826,
7	13	44.8	25	12	US-11-136-527-105827	Sequence 105827,
8	13	44.8	25	12	US-11-136-527-105834	Sequence 105834,
9	13	44.8	25	12	US-11-136-527-105835	Sequence 105835,
10	13	44.8	25	12	US-11-136-527-307733	Sequence 307733,
11	13	44.8	25	12	US-11-136-527-307741	Sequence 307741,
12	13	44.8	50	12	US-11-175-859-37597	Sequence 37597, A
13	13	44.8	63	9	US-11-173-887-37	Sequence 37, Appl
14	13	44.8	63	9	US-11-173-887-49	Sequence 49, Appl
c 15	12	41.4	18	8	US-10-310-914A-1107332	Sequence 1107332,
16	12	41.4	19	8	US-10-310-914A-811205	Sequence 811205,
17	12	41.4	19	10	US-11-101-244-79718	Sequence 79718, A
18	12	41.4	19	10	US-11-101-244-79729	Sequence 79729, A
19	12	41.4	19	10	US-11-101-244-79757	Sequence 79757, A
20	12	41.4	19	10	US-11-101-244-79763	Sequence 79763, A
c 21	12	41.4	19	10	US-11-101-244-118485	Sequence 118485,
c 22	12	41.4	19	10	US-11-101-244-139751	Sequence 139751,
23	12	41.4	19	10	US-11-101-244-165432	Sequence 165432,
24	12	41.4	19	10	US-11-101-244-165442	Sequence 165442,
25	12	41.4	19	10	US-11-101-244-165526	Sequence 165526,
26	12	41.4	19	10	US-11-101-244-333291	Sequence 333291,
27	12	41.4	19	10	US-11-101-244-360130	Sequence 360130,
28	12	41.4	19	10	US-11-101-244-360145	Sequence 360145,
29	12	41.4	19	10	US-11-101-244-360149	Sequence 360149,
30	12	41.4	19	10	US-11-101-244-490989	Sequence 490989,
31	12	41.4	19	10	US-11-101-244-491087	Sequence 491087,
c 32	12	41.4	19	10	US-11-101-244-581754	Sequence 581754,
33	12	41.4	19	10	US-11-101-244-1192442	Sequence 1192442,
34	12	41.4	19	10	US-11-101-244-1192476	Sequence 1192476,
35	12	41.4	19	10	US-11-101-244-1192502	Sequence 1192502,
c 36	12	41.4	19	10	US-11-101-244-1195364	Sequence 1195364,
37	12	41.4	19	10	US-11-101-244-1255833	Sequence 1255833,
38	12	41.4	19	10	US-11-101-244-1306392	Sequence 1306392,
39	12	41.4	19	10	US-11-101-244-1472078	Sequence 1472078,
40	12	41.4	19	11	US-11-083-784-79718	Sequence 79718, A
41	12	41.4	19	11	US-11-083-784-79729	Sequence 79729, A
42	12	41.4	19	11	US-11-083-784-79757	Sequence 79757, A
43	12	41.4	19	11	US-11-083-784-79763	Sequence 79763, A
c 44	12	41.4	19	11	US-11-083-784-118485	Sequence 118485,
c 45	12	41.4	19	11	US-11-083-784-139751	Sequence 139751,

ALIGNMENTS

RESULT 1
US-11-101-244-1039686
; Sequence 1039686, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1039686
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1039686

Query Match 44.8%; Score 13; DB 10; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy          8 AGGTTACCATAGA 20
              |||::||||:|||
Db          7 AGGUUACCAUAGA 19
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RESULT 2
US-11-083-784-1039686
; Sequence 1039686, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1039686
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1039686

Query Match 44.8%; Score 13; DB 11; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGGTTACCATAGA 20
||::||||:|||
Db 7 AGGUUACCAUAGA 19

RESULT 3
US-11-121-849-210096
; Sequence 210096, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-210096

Query Match 44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGGTTACCATAGA 20
||||||||||||
Db 7 AGGTTACCATAGA 19

RESULT 4
US-11-121-849-235837/c
; Sequence 235837, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235837

Query Match 44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 CCATAGAGCCACT 26
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Db 14 CCATAGAGCCACT 2

RESULT 5
US-11-121-849-417792/c
; Sequence 417792, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 417792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-417792

Query Match 44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CAGAGGTTACCAT 17
||||||||||||
Db 24 CAGAGGTTACCAT 12

RESULT 6
US-11-136-527-105826
; Sequence 105826, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105826
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-105826

Query Match 44.8%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db          1 TACCATAGAGCCA 13


RESULT 7
US-11-136-527-105827
; Sequence 105827, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105827
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-105827

  Query Match            44.8%;  Score 13;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db          2 TACCATAGAGCCA 14


RESULT 8
US-11-136-527-105834
; Sequence 105834, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105834
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-105834

  Query Match            44.8%;  Score 13;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db          3 TACCATAGAGCCA 15


RESULT 9
US-11-136-527-105835
; Sequence 105835, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105835
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-105835

  Query Match            44.8%;  Score 13;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db          5 TACCATAGAGCCA 17


RESULT 10
US-11-136-527-307733
; Sequence 307733, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 307733
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-307733

  Query Match            44.8%;  Score 13;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db         11 TACCATAGAGCCA 23


RESULT 11
US-11-136-527-307741
; Sequence 307741, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
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;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 307741
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Probe
US-11-136-527-307741

  Query Match             44.8%;  Score 13;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db         10 TACCATAGAGCCA 22


RESULT 12
US-11-175-859-37597
; Sequence 37597, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
;  APPLICANT: Affymetrix, Inc.
;  APPLICANT:  Liu, Guoying et al.
;  TITLE OF INVENTION: Method of Analysis of Human Polymorphism
;  FILE REFERENCE: 3690.1
;  CURRENT APPLICATION NUMBER: US/11/175,859
;  CURRENT FILING DATE:  2005-07-05
;  PRIOR APPLICATION NUMBER: US 60/585,352
;  PRIOR FILING DATE: 2004-07-02
;  NUMBER OF SEQ ID NOS: 116251
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37597
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: homo sapien
US-11-175-859-37597

  Query Match             44.8%;  Score 13;  DB 12;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db         31 TACCATAGAGCCA 43


RESULT 13
US-11-173-887-37
; Sequence 37, Application US/11173887
; Publication No. US20060029954A1
; GENERAL INFORMATION:
;  APPLICANT: LAO, KAI QIN
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING NUCLEOTIDES IN
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 375461-017US
;  CURRENT APPLICATION NUMBER: US/11/173,887
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/584,643
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
;   LENGTH: 63
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primer
US-11-173-887-37

  Query Match             44.8%;  Score 13;  DB 9;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCA 16
              |||||||||||||
Db         44 TCAGAGGTTACCA 56


RESULT 14
US-11-173-887-49
; Sequence 49, Application US/11173887
; Publication No. US20060029954A1
; GENERAL INFORMATION:
;  APPLICANT: LAO, KAI QIN
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING NUCLEOTIDES IN
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 375461-017US
;  CURRENT APPLICATION NUMBER: US/11/173,887
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/584,643
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
;   LENGTH: 63
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primer
US-11-173-887-49

  Query Match             44.8%;  Score 13;  DB 9;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCA 16
              |||||||||||||
Db         44 TCAGAGGTTACCA 56


RESULT 15
US-10-310-914A-1107332/c
; Sequence 1107332, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
;  APPLICANT: Bentwich, Isaac
;  APPLICANT:  Shiler, Kvuzat
;  TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
;  TITLE OF INVENTION:  uses thereof
;  FILE REFERENCE: 06087.0200.CPUS01
;  CURRENT APPLICATION NUMBER: US/10/310,914A
;  CURRENT FILING DATE:  2002-12-06
;  NUMBER OF SEQ ID NOS: 1388402
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1107332
;   LENGTH: 18
;   TYPE: RNA
;   ORGANISM: Human
US-10-310-914A-1107332

  Query Match             41.4%;  Score 12;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CAGAGGTTACCA 16
              ||||||||||||
Db         16 CAGAGGTTACCA 5
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Search completed: March 5, 2006, 22:48:30
Job time : 450.5 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:52:50 ; Search time 907 Seconds
(without alignments)
1817.486 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27.4	94.5	673	13	DQ003076	DQ003076 Human pap
2	27.4	94.5	1546	13	AF070938	AF070938 Human pap
3	27.4	94.5	3891	13	HPU40822	U40822 Human papil
4	27.4	94.5	7759	13	HPU37488	U37488 Human papil
5	27.4	94.5	7887	13	AF436130	AF436130 Human pap
6	27.4	94.5	7889	13	AF020905	AF020905 Common ch
7	27.4	94.5	7966	13	AF419318	AF419318 Human pap
8	27.4	94.5	7975	13	AJ620205	AJ620205 Human pap
9	25.8	89.0	38	6	I17042	I17042 Sequence 53
10	25.8	89.0	38	6	BD017550	BD017550 Short-cha
11	25.8	89.0	386	6	A91822	A91822 Sequence 2
12	25.8	89.0	386	6	AR216808	AR216808 Sequence
c 13	25.8	89.0	386	6	AR216809	AR216809 Sequence
14	25.8	89.0	386	6	BD023226	BD023226 Papilloma
15	25.8	89.0	386	13	HPVZ95953	Z95953 Human papil
16	25.8	89.0	587	13	DQ003068	DQ003068 Human pap
17	25.8	89.0	807	13	DQ003075	DQ003075 Human pap
18	25.8	89.0	927	13	DQ003078	DQ003078 Human pap
19	25.8	89.0	929	13	DQ003070	DQ003070 Human pap
20	25.8	89.0	1421	6	AX452915	AX452915 Sequence
21	25.8	89.0	1497	6	CS103057	CS103057 Sequence
22	25.8	89.0	1524	6	AR047985	AR047985 Sequence
23	25.8	89.0	1524	6	AR059325	AR059325 Sequence
24	25.8	89.0	1524	6	CQ815809	CQ815809 Sequence
25	25.8	89.0	1575	13	AY101598	AY101598 Human pap
26	25.8	89.0	1607	13	AY863156	AY863156 Human pap
27	25.8	89.0	1607	13	AY863157	AY863157 Human pap
28	25.8	89.0	1607	13	AY863158	AY863158 Human pap
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31	25.8	89.0	1607	13	AY863161	AY863161 Human pap
32	25.8	89.0	1607	13	AY863162	AY863162 Human pap
33	25.8	89.0	1607	13	AY863163	AY863163 Human pap
34	25.8	89.0	1607	13	AY863164	AY863164 Human pap
35	25.8	89.0	1607	13	AY863165	AY863165 Human pap
36	25.8	89.0	5210	13	HPU89349	U89349 Human papil
37	25.8	89.0	7184	13	HPU31790	U31790 Human papil
38	25.8	89.0	7717	13	AF436129	AF436129 Human pap
39	25.8	89.0	7824	6	CS073242	CS073242 Sequence
40	25.8	89.0	7824	13	PPH58	D90400 Human papil
41	25.8	89.0	7857	6	CS073239	CS073239 Sequence
42	25.8	89.0	7857	13	AY262282	AY262282 Human pap
43	25.8	89.0	7857	13	PAPHPV18	X05015 Human papil
44	25.8	89.0	7880	13	HPVT13DNA	X62843 Human papil
45	25.8	89.0	7896	13	HPV59VG	X77858 Human papil

ALIGNMENTS

RESULT 1
DQ003076
LOCUS DQ003076 673 bp DNA linear VRL 15-AUG-2005
DEFINITION Human papillomavirus type 54 nonfunctional L1 gene, partial sequence.
ACCESSION DQ003076
VERSION DQ003076.1 GI:66866335
KEYWORDS .
SOURCE Human papillomavirus - 54
ORGANISM Human papillomavirus - 54
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE 1 (bases 1 to 673)
AUTHORS Wu,X., Ren,J., Ran,D. and Ma,R.Z.
TITLE Detection of HPV types in cervical brush samples of clinical patients in Beijing and other Northern China cities
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 673)
AUTHORS Wu,X., Ren,J. and Ma,R.Z.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2005) Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, A5 Datun Raod, Chaoyang District, Beijing 100101, China
FEATURES Location/Qualifiers
source 1. .673
/organism="Human papillomavirus - 54"
/mol_type="genomic DNA"
/isolation_source="epithelial cells from cervix"
/sub_species="54"
/db_xref="taxon:333766"
/country="China"
misc_feature <1. .>673
/note="nonfunctional L1 due to mutation"
ORIGIN

Query Match 94.5%; Score 27.4; DB 13; Length 673;
Best Local Similarity 96.6%; Pred. No. 0.98;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
|||||||||||||||||||| |||||||||

```
Db        530 GATGGTGATATGGTAGATATAGGATTTGG 558


RESULT 2
AF070938
LOCUS       AF070938               1546 bp    DNA     linear   VRL 30-SEP-1998
DEFINITION  Human papillomavirus late major capsid protein (L1) gene, complete
            cds.
ACCESSION   AF070938
VERSION     AF070938.1  GI:3676538
KEYWORDS    .
SOURCE      Human papillomavirus
  ORGANISM  Human papillomavirus
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Feoli-Fonseca,J.C., Oligny,L.L., Filion,M., Simard,P., Russo,P.A.
            and Yotov,W.V.
  TITLE     JC9813-A putative novel human papillomavirus identified by PCR-DS
  JOURNAL   Biochem. Biophys. Res. Commun. 250 (1), 63-67 (1998)
   PUBMED   9735332
REFERENCE   2  (bases 1 to 1546)
  AUTHORS   Feoli-Fonseca,J.C., Oligny,L.L., Filion,M., Simard,P., Russo,P.A.
            and Yotov,W.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUN-1998) Cancer Center Charles Bruneau, Hospital
            Ste-Justine, 3175 Cote Ste-Catherine, Montreal, QC H3T 1C5, Canada
FEATURES             Location/Qualifiers
     source          1. .1546
                     /organism="Human papillomavirus"
                     /mol_type="genomic DNA"
                     /strain="JC9813"
                     /db_xref="taxon:10566"
                     /note="identified in 1997 in a cervical biopsy from a
                     38-year old English Canadian woman, HIV-positive since
                     1988; pathological diagnosis LSIL"
     gene            8. .1516
                     /gene="L1"
     CDS             8. .1516
                     /gene="L1"
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                     /product="late major capsid protein"
                     /protein_id="AAC62011.1"
                     /db_xref="GI:3676539"
                     /translation="MWRLNDNKVYLPPPGPIASIVSTDEYVQRTNLFYHAGSSRLLAV
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                     VEIGRGQPLGVGISGHPYLNKYDDIENPSGYGTSPGQDNRENVAMDYKQTQLCIVGCT
                     PPMGEYWGKGVPCSTSGITQGDCPVIELKSEVIEDGDMVDTGFGALDFASLQASKSDV
                     PLDLCNTKSKYPDYLGMAAEPYGNSLFFFLRREQMFVRHFFNKAGTTGDAVPQDLYIA
                     GTGNRAKIAGSIYYSTPSGSLVTSDSQLFNKPLWMQKAQGHNNGICFGNQVFVTVVDT
                     TRSTNLTLCASTESVLPTTYDNTKFKEYLRHAEEFDLQFIFQLCIITLNPEVMTYIHT
                     MDASLLEDWNFGVSPPSHGSLEDTYRFLANKAITCQKNVPPKAKEDPYKNYTFWDVDL
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ORIGIN

  Query Match           94.5%;  Score 27.4;  DB 13;  Length 1546;
  Best Local Similarity   96.6%;  Pred. No. 0.9;
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Db        590 GATGGTGATATGGTAGATACAGGGTTTGG 618


RESULT 3
HPU40822
LOCUS       HPU40822               3891 bp    DNA     linear   VRL 15-AUG-1996
DEFINITION  Human papillomavirus type 74 E6 protein (E6), E7 protein (E7), and
            L1 protein (L1) genes, complete cds.
ACCESSION   U40822
VERSION     U40822.1  GI:1491796
KEYWORDS    .
SOURCE      Human papillomavirus type 74
  ORGANISM  Human papillomavirus type 74
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 3891)
  AUTHORS   Longuet,M., Cassonnet,P. and Orth,G.
  TITLE     A novel genital human papillomavirus (HPV), HPV type 74, found in
            immunosuppressed patients
  JOURNAL   J. Clin. Microbiol. 34 (7), 1859-1862 (1996)
   PUBMED   8784613
REFERENCE   2  (bases 1 to 3891)
  AUTHORS   Longuet,M., Cassonnet,P. and Orth,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1995) Michele Longuet, Laboratoire des
            Papillomavirus, Institut Pasteur, 25 Rue du Dr Roux, Paris 75015,
            France
FEATURES             Location/Qualifiers
     source          1. .3891
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:44028"
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                     KVISTDAYVTRTNIFYHASSSRLLAVGNPYFPIRQSNKTVVPKVSGYQFRVFKVVLPD
                     PNKFALPDTSIFDPSSQRLVWACTGLEVGRGQPLGIGISGHPLLNKLDDVENSASYAA
                     NPGQDNRVNVAMDYKQTQLCMVGCAPPLGEHWGKGKQCSNVNVKPGDCPALELITSVI
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                     QMFARHFFNRAGTVGEDIPQDLYIKGTTRSTLANAIYFNTPSGSLVSSETQLFNKPFW
                     LQRAQGHNNGICWGNQLFVTVVDTTRSTNMTVCAPTSQSPSATYNSSDYKQYMRHVEE
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     gene            2948. .3400
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     CDS             2948. .3400
                     /gene="E6"
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                     /codon_start=1
                     /product="E6 protein"
                     /protein_id="AAC55127.1"
                     /db_xref="GI:1491798"
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ORIGIN

  Query Match           94.5%;  Score 27.4;  DB 13;  Length 3891;
  Best Local Similarity   96.6%;  Pred. No. 0.82;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       1239 GATGGTGATATGGTAGATACAGGCTTTGG 1267
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RESULT 4
HPU37488
LOCUS       HPU37488                7759 bp    DNA     linear   VRL 06-DEC-1999
DEFINITION  Human papillomavirus type 54, complete genome.
ACCESSION   U37488
VERSION     U37488.1  GI:1017782
KEYWORDS    .
SOURCE      Human papillomavirus - 54
  ORGANISM  Human papillomavirus - 54
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7759)
  AUTHORS   Delius,H.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7759)
  AUTHORS   Farmer,A.D.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-OCT-1995) Andrew Farmer, Los Alamos National
            Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
            Alamos, NM 87501 USA
COMMENT     HPV-54 was first isolated from a patient with condyloma acuminata.
FEATURES             Location/Qualifiers
     source          1. .7759
                     /organism="Human papillomavirus - 54"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:333766"
     gene            102. .536
                     /gene="E6"
     CDS             102. .536
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                     /protein_id="AAA79187.1"
                     /db_xref="GI:1017783"
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     gene            536. .823
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     CDS             536. .823
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                     /codon_start=1
                     /product="transforming protein"
                     /protein_id="AAA79188.1"
                     /db_xref="GI:1017784"
                     /translation="MHGNVATIEDIVLDLKPEPFDLYCREQLEDSDAEDETAVTQPDK
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                     /db_xref="GI:1017785"
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                     QTVSGETTTDSLGRQQITELIHNTNIRVALFGMFKDLYGLSFMDLARPFKSDKTVCTD
                     WVIAAFGIYHGITDGFKTLLEPHCLYGHIQWLTCRWGMVLLLLTRFKCGKNRLTVSKC
                     LGMLLNIPETQMLIDPPKLRTPAAALYWYRQGLSNASEIFGTPPEWLARQTVIEYSLA
                     DSQFDLSKMVQWAYDHNYIDDSIIALEYAKLADIDENAAAFLGSNCQAKYVKDCGTMC
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                     /db_xref="GI:1017786"
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                     YMDAEHKVYYVDFKKEASKYGEYGQWEVRMGSSIIFSPASVSSTEEALSISSTGTAEH
                     TRPANSTPRTDNSTKAIPCTPPPRKRARVYSTDQQPHSTSDPVGCDNDRHISDDNNKN
                     QGRHTSSGDTTPIVHFKGEPNTLKCFRQRIQKYKHLFEQASSTWHWACVPGTTKNRGI
                     VTLTYSSVEQRQQFLVTVRIPPSISMSLGVMSL"
     gene            3134. .3538
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     CDS             3134. .3538
                     /gene="E4"
                     /note="putative; ORF E4 from bp 3134 to 3538"
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                     /protein_id="AAA79191.1"
                     /db_xref="GI:1017787"
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     gene            4215. .5627
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                     IYTEPSLLDPPPPVQMDGRVLVSTSTLQSSTAENIPMDTFIIMQDHIGTTTSTPIPRP
                     PARPRLGLYSRALQQVPVQDPAFLQQPSSLITYDNPVYEGNPDVTLHFEQPTIHNAPD
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                     EIELHPLISANNTSINNGLYSDIYDVYADTDFADTGGFSSSTVSHSSVQTALQTTSIP
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     gene            5614. .7107
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ORIGIN

  Query Match             94.5%;  Score 27.4;  DB 13;  Length 7759;
  Best Local Similarity   96.6%;  Pred. No. 0.76;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db       6190 GATGGTGATATGGTAGATATAGGATTTGG 6218


RESULT 5
AF436130
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LOCUS       AF436130               7887 bp    DNA     linear   VRL 02-JAN-2003
DEFINITION  Human papillomavirus type 74 subtype AE10, complete genome.
ACCESSION   AF436130
VERSION     AF436130.1  GI:27462483
KEYWORDS    .
SOURCE      Human papillomavirus type 74
  ORGANISM  Human papillomavirus type 74
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7887)
  AUTHORS   Terai,M. and Burk,R.D.
  TITLE     Cervical HPVs in Evolution; Genomic sequence of AE10, a Subtype of
            HPV74
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7887)
  AUTHORS   Burk,R.D. and Terai,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2001) Microbiology & Immunology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, New York, NY
            10461, USA
FEATURES             Location/Qualifiers
     source          1. .7887
                     /organism="Human papillomavirus type 74"
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     CDS             1. .453
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                     /protein_id="AAO15456.1"
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                     KNRCTVARMLATLLNIPEDHMLIEPPKIQSTVAALYWFRSSLSNASIVQGDTPDWITR
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                     EAPCVSQTETPWTVQTTTSSLTITTITKDGTTVTVELRL"
     gene            3762. .4037
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                     /protein_id="AAO15460.1"
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                     SILVLTLILYLLLWLLLTSALQFYTLTLCVCYLPAFSLHLYILHNLE"
     gene            4210. .5604
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                     /product="putative minor capsid protein L2"
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                     SIVSLVEESAIINSGAPEVVPPSHGGFEITTSESTTPAILDVSVTTHNTTSTSVFRNP
                     SFTDPSVIQSQPPVEAGGHVLISSSTVSSHPVEEIPLDTFIVSSSDSNPASSTPIPTA
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                     NPGQDNRVNVAMDYKQTQLCMVGCAPPLGEHWGKGKQCSNVTVKPGDCPALELITSVI
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ORIGIN

  Query Match            94.5%;  Score 27.4;  DB 13;  Length 7887;
  Best Local Similarity  96.6%;  Pred. No. 0.76;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||||||||||| |||||
Db       6170 GATGGTGATATGGTAGATACAGGCTTTGG 6198
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RESULT 6
AF020905
LOCUS       AF020905               7889 bp    DNA     linear   VRL 01-OCT-1997
DEFINITION  Common chimpanzee papillomavirus 1, complete genome.
ACCESSION   AF020905
VERSION     AF020905.1  GI:2454637
KEYWORDS    .
SOURCE      Common chimpanzee papillomavirus 1
  ORGANISM  Common chimpanzee papillomavirus 1
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae; primate papillomaviruses; Common
            chimpanzee papillomavirus.
REFERENCE   1  (bases 1 to 7889)
  AUTHORS   Scinicariello,F., Soza,I., Brasky,K.M. and Hilliard,J.K.
  TITLE     DNA sequence of a novel papillomavirus (CCPV1) from an outbreak of
            focal epithelial hyperplasia-like disease in a common chimpanzee
            (Pan troglodytes) colony
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7889)
  AUTHORS   Scinicariello,F., Soza,I., Brasky,K.M. and Hilliard,J.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-1997) Yerkes Primate Research Center, Emory
            University, 954 Gatewood Dr NE, Atlanta, GA 30322, USA
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ORIGIN

  Query Match             94.5%;  Score 27.4;  DB 13;  Length 7889;
  Best Local Similarity   96.6%;  Pred. No. 0.76;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 7
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DEFINITION  Human papillomavirus type 91, complete genome.
ACCESSION   AF419318
VERSION     AF419318.1  GI:22023568
KEYWORDS    .
SOURCE      Human papillomavirus - cand91 (candHPV91)
  ORGANISM  Human papillomavirus - cand91
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7966)
  AUTHORS   Terai,M. and Burk,R.D.
  TITLE     Identification and Characterization of 3 Novel Genital Human
            Papillomaviruses by Overlapping Polymerase Chain Reaction:
            candHPV89, candHPV90, and candHPV91
  JOURNAL   J. Infect. Dis. 185 (12), 1794-1797 (2002)
   PUBMED   12085327
REFERENCE   2  (bases 1 to 7966)
  AUTHORS   Burk,R.D. and Terai,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-2001) Microbiology & Immunology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, New York, NY
            10461, USA
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ORIGIN

  Query Match             94.5%;  Score 27.4;  DB 13;  Length 7966;
  Best Local Similarity   96.6%;  Pred. No. 0.76;
  Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 8
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LOCUS       AJ620205               7975 bp    DNA     circular VRL 15-APR-2005
DEFINITION  Human papillomavirus type 43 complete genome.
ACCESSION   AJ620205
VERSION     AJ620205.1  GI:40804474
KEYWORDS    E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; L1 gene; L2 gene; X
            gene; Y gene.
SOURCE      Human papillomavirus type 43
  ORGANISM  Human papillomavirus type 43
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1
  AUTHORS   Lorincz,A.T., Quinn,A.P., Goldsborough,M.D., Schmidt,B.J. and
            Temple,G.F.
  TITLE     Cloning and partial DNA sequencing of two new human papillomavirus
            types associated with condylomas and low-grade cervical neoplasia
  JOURNAL   J. Virol. 63 (6), 2829-2834 (1989)
   PUBMED   2542593
REFERENCE   2
  AUTHORS   Matsukura,T., Delius,H. and Sugase,M.
  TITLE     Cloning and sequencing of the full-length genome of HPV 43
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 7975)
  AUTHORS   de Villiers,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-2004) de Villiers E.M., Div. Characterization of
            Tumorviruses, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld
            242, Heidelberg, 69120, GERMANY
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                /codon_start=1
                /product="L1 protein"
                /protein_id="CAF05789.1"
                /db_xref="GI:40804481"
                /db_xref="GOA:Q705H4"
                /db_xref="InterPro:IPR000583"
                /db_xref="InterPro:IPR002210"
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                /translation="MALIFICILHCGIWANAVNAFHIFLQITMWRLNDNKVYLPPPGP
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                LPDPNKFGFSETTLVTSDTQRLVWGCVGVEIGRGQPLGVGISGHPYLNKYDDTENPSG
                YGTSPGQDNRENVAMDYKQTQLCIVGCTPPMGEYWGQGVPCNASGVTQGDCPVIELKS
                EVIQDGDMVDTGFGAMDFASLQASKSDVPLDLVNTKSKYPDYLGMAAEPYGNSLFFFL
                RREQMFLRHFFNKAGKTGDVVPSDMYIAGSNTRSKIADSIYFSTPSGSLVTSDSQLFN
                KPLWIQKAQGHNNGICFGNQLFVTVVDTTRSTNLTLCASTDPTVPSTYDNAKFKEYLR
                HVEEYDLQFIFQLCIITLNPEVMTYIHTMDPTLLEDWNFGVSPPASASLEDTYRFLSN
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                /db_xref="UniProt/TrEMBL:Q705H3"
                /translation="MWRLNDNKVYLPPPGPIASIVSTDEYVQRTNLFYYAGSSRLLAV
                GHPYFPLKNSSGKITVPKVSGYQYRVFRVKLPDPNKFGFSETTLVTSDTQRLVWGCVG
                VEIGRGQPLGVGISGHPYLNKYDDTENPSGYGTSPGQDNRENVAMDYKQTQLCIVGCT
                PPMGEYWGQGVPCNASGVTQGDCPVIELKSEVIQDGDMVDTGFGAMDFASLQASKSDV
                PLDLVNTKSKYPDYLGMAAEPYGNSLFFFLRREQMFLRHFFNKAGKTGDVVPSDMYIA
                GSNTRSKIADSIYFSTPSGSLVTSDSQLFNKPLWIQKAQGHNNGICFGNQLFVTVVDT
                TRSTNLTLCASTDPTVPSTYDNAKFKEYLRHVEEYDLQFIFQLCIITLNPEVMTYIHT
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                /translation="MGIVCFFFYAGNKCSLDIFLIKLVKLATLCLPICILLALIPGPK,
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                PLCFITFLFFLTYIFVFHSY"

Query Match             94.5%;  Score 27.4;  DB 13;  Length 7975;
Best Local Similarity   96.6%;  Pred. No. 0.76;
Matches   28;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||| ||||||||||||||||||||
Db       6339 GATGGTGACATGGTAGATACAGGATTTGG 6367


RESULT 9
I17042
LOCUS       I17042                    38 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 53 from patent US 5484699.
ACCESSION   I17042
VERSION     I17042.1  GI:1251950
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Bouma,S.R., Joseph,J.L., Marshall,R.L. and Laffler,T.G.
  TITLE     Nucleotide sequences useful as type specific probes, PCR primers
            and LCR probes for the amplification and detection of human
            papilloma virus, and related kits and methods
  JOURNAL   Patent: US 5484699-A 53 16-JAN-1996;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   93.1%;  Pred. No. 6.1;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| |||||||| |||||
Db          1 GATGGTGATATGGTTGATACAGGCTTTGG 29


RESULT 10
BD017550
LOCUS       BD017550                  38 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Short-chain nucleotide sequence of human papilloma virus.
ACCESSION   BD017550
VERSION     BD017550.1  GI:22558726
KEYWORDS    JP 2001231587-A/53.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Joseph,J.L., Borma,S.R., Marshall,R.L. and Rahler,T.G.
  TITLE     Short-chain nucleotide sequence of human papilloma virus
  JOURNAL   Patent: JP 2001231587-A 53 28-AUG-2001;
            ABBOTT LABORATORIES
COMMENT     OS   Unidentified
            PN   JP 2001231587-A/53
            PD   28-AUG-2001
            PF   31-JAN-2001 JP 2001023849
            PR   28-SEP-1990 US       589948,28-SEP-1990 US       590105 PR
            28-SEP-1990 US       590253
            PI   JEFFREY L JOSEPH,STANLEY R BORMA,RONALD L MARSHALL,THOMAS G
            PI   RAHLER
            PC   C12N15/09,C12M1/00,C12Q1/68//(C12N15/09,C12R1:93),C12N15/00,
            PC   (C12N15/00,C12R1:93)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Short-chain nucleotide sequence of human papilloma virus FH
            Key             Location/Qualifiers
            FT   source          1. .38
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN
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  Best Local Similarity   93.1%;  Pred. No. 6.1;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| |||||||| |||||
Db          1 GATGGTGATATGGTTGATACAGGCTTTGG 29


RESULT 11
A91822
LOCUS       A91822                  386 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9823752.
ACCESSION   A91822
VERSION     A91822.1  GI:6740700
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Zur,H.H. and Lavergne,D.
  TITLE     PAPILLOMA VIRUSES, AGENTS FOR DETECTING THE SAME AND FOR TREATING
            DISEASES CAUSED BY SUCH VIRUSES
  JOURNAL   Patent: WO 9823752-A 2 04-JUN-1998;
            DEUTSCHES KREBSFORSCH (DE); ZUR HAUSEN HARALD (DE)
FEATURES             Location/Qualifiers
     source          1. .386
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             <1. .>384
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAB69436.1"
                     /db_xref="GI:6740701"
                     /translation="IEDGDMVDIGFGNCNFKALQQDKAGTPLELTNEKCKWPDFLKME
                     KDTYGDQMFFCGRKEQMYSRHMLAKAGIDGDHIPESLYHSPKNNGNGIAPYTYFPTTS
                     GSLVTSDNQLFNRPYWLHNSQGTNNG"
ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 6;  Length 386;
  Best Local Similarity   93.1%;  Pred. No. 4.8;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||| | |||||||||
Db          7 GATGGTGATATGGTAGACATAGGATTTGG 35


RESULT 12
AR216808
LOCUS       AR216808                386 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6413522.
ACCESSION   AR216808
VERSION     AR216808.1  GI:23316083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   De Villiers-Zur Hausen,E.-M., Zur Hausen,H., Lavergne,D. and
            Benton,C.
  TITLE     Papilloma viruses, products for the detection thereof as well as
            for treating diseases caused by them
  JOURNAL   Patent: US 6413522-A 4 02-JUL-2002;
            Deutsches Krebsforschungszentrum Stiftung des Offentlichen Rechts;
            Heidelberg;
            WOX;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 6;  Length 386;
  Best Local Similarity   93.1%;  Pred. No. 4.8;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||| | |||||||||
Db          7 GATGGTGATATGGTAGACATAGGATTTGG 35


RESULT 13
AR216809/c
LOCUS       AR216809                386 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 6 from patent US 6413522.
ACCESSION   AR216809
VERSION     AR216809.1  GI:23316084
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   De Villiers-Zur Hausen,E.-M., Zur Hausen,H., Lavergne,D. and
            Benton,C.
  TITLE     Papilloma viruses, products for the detection thereof as well as
            for treating diseases caused by them
  JOURNAL   Patent: US 6413522-A 6 02-JUL-2002;
            Deutsches Krebsforschungszentrum Stiftung des Offentlichen Rechts;
            Heidelberg;
            WOX;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||| | |||||||||
Db        380 GATGGTGATATGGTAGACATAGGATTTGG 352


RESULT 14
BD023226
LOCUS       BD023226                386 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Papilloma virus, reagent for detecting the virus and reagent for
            treating diseases caused by the virus.
ACCESSION   BD023226
VERSION     BD023226.1  GI:22564449
KEYWORDS    JP 2001505767-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Zur,E.M.D.V., Hausen,H.Z., Lavergne,D. and Benton,C.
  TITLE     Papilloma virus, reagent for detecting the virus and reagent for
            treating diseases caused by the virus
  JOURNAL   Patent: JP 2001505767-A 2 08-MAY-2001;
            DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT     PN   JP 2001505767-A/2
            PD   08-MAY-2001
            PF   12-NOV-1997 JP 1998524126
            PR   26-NOV-1996 DE   19648962.8
            PI   ETHEL MICHELE DE VILLIERS ZUR HAUSEN,HARALD ZUR HAUSEN,DONNA
            PI   LAVERGNE,
            PI   CLAIRE BENTON
            PC   C12N15/09,A61K38/00,A61K39/12,A61K39/395,A61K39/395,A61K48/00,
            PC   A61P31/20,
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            PC   C07K14/025,C07K16/08,C12N1/19,C12N1/21,C12N5/10,C12Q1/68, PC
            C12N15/00,
            PC   C12N5/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /desc = 'DNA'
            FH   Key             Location/Qualifiers
            FT   CDS             1. .384.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 6;  Length 386;
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  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||||| | |||||||||
Db          7 GATGGTGATATGGTAGACATAGGATTTGG 35


RESULT 15
HPVZ95953
LOCUS       HPVZ95953               386 bp    DNA     linear   VRL 07-NOV-2004
DEFINITION  Human papillomavirus DNA for partial HPV L1 sequence.
ACCESSION   Z95953
VERSION     Z95953.1  GI:2664381
KEYWORDS    L1.
SOURCE      Human papillomavirus
  ORGANISM  Human papillomavirus
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   de Villiers,E.M., Lavergne,D., McLaren,K. and Benton,E.C.
  TITLE     Prevailing papillomavirus types in non-melanoma carcinomas of the
            skin in renal allograft recipients
  JOURNAL   Int. J. Cancer 73 (3), 356-361 (1997)
   PUBMED   9359482
REFERENCE   2  (bases 1 to 386)
  AUTHORS   de Villiers,E.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-MAY-1997) de Villiers E.M., Deutsches
            Krebsforschungszentrum, Tumorvirus Charakterisierung 0660, Im
            Neuenheimer Feld 242, 69120, Heidelberg, Germany
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="Human papillomavirus"
                     /mol_type="genomic DNA"
                     /isolate="isolated from Skin squamous cell carcinoma
                     biopsy, WV-9021; partial HPV L1 seque"
                     /specific_host="Homo sapiens"
                     /db_xref="taxon:10566"
                     /clone_lib="DL20"
     repeat_region   117. .123
ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 13;  Length 386;
  Best Local Similarity   93.1%;  Pred. No. 4.8;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||||| | |||||||||
Db          7 GATGGTGATATGGTAGACATAGGATTTGG 35


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GenCore version 5.1.7

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	29	12	ADQ27974	Adq27974 Human pap
2	25.8	89.0	38	2	AAQ23183	Aaq23183 HPV probe
3	25.8	89.0	38	2	AAT29878	Aat29878 Human pap
4	25.8	89.0	386	2	AAV15595	Aav15595 Papilloma
5	25.8	89.0	1421	6	AAL47486	Aal47486 HPV type
6	25.8	89.0	1497	14	AEA12674	Aea12674 DNA encod
7	25.8	89.0	1524	2	AAT40119	Aat40119 Human pap
8	25.8	89.0	1950	2	AAQ04472	Aaq04472 Human pap
9	25.8	89.0	2017	1	AAN91804	Aan91804 Human pap
10	25.8	89.0	7824	14	ADZ45651	Adz45651 Human pap
11	25.8	89.0	7857	14	ADZ45648	Adz45648 Human pap
12	25.8	89.0	7880	12	ADN12113	Adn12113 HPV type
13	25.8	89.0	7896	12	ADN12111	Adn12111 HPV type
14	24.2	83.4	410	2	AAT47256	Aat47256 (DSM 1009
15	24.2	83.4	1422	12	ADF89368	Adf89368 Plant-opt
16	24.2	83.4	1443	12	ADF89363	Adf89363 Plant-opt
17	24.2	83.4	1452	10	ACC47503	Acc47503 HPV 16 L1
18	24.2	83.4	1452	10	ACC47505	Acc47505 HPV 16 L1
19	24.2	83.4	1494	3	AAD01237	Aad01237 Chimeric
20	24.2	83.4	1500	3	AAD01238	Aad01238 Chimeric
21	24.2	83.4	1506	12	ADF89361	Adf89361 Plant-opt
22	24.2	83.4	1515	13	ADS16246	Ads16246 Human pap
23	24.2	83.4	1515	13	ADS16247	Ads16247 Human pap
24	24.2	83.4	1517	2	AAQ47167	Aaq47167 HPV1 L1 O
25	24.2	83.4	1517	2	AAV09856	Aav09856 HPV16 rec
26	24.2	83.4	1517	2	AAV25817	Aav25817 Human pap
27	24.2	83.4	1517	2	AAV12161	Aav12161 Human pap
28	24.2	83.4	1517	2	AAV24099	Aav24099 HPV16 L1
29	24.2	83.4	1517	2	AAX15112	Aax15112 Human pap
30	24.2	83.4	1517	3	AAZ40564	Aaz40564 HPV16 L1
31	24.2	83.4	1517	10	ADC26169	Adc26169 HPV16 L1
32	24.2	83.4	1517	12	ADG62855	Adg62855 Human pap
33	24.2	83.4	1518	2	AAX37566	Aax37566 Human pap
34	24.2	83.4	1518	3	AAZ48174	Aaz48174 Human pap
35	24.2	83.4	1518	6	ABL58976	Abl58976 HPV16-L1
36	24.2	83.4	1518	9	ABX11395	Abx11395 Human pap
37	24.2	83.4	1518	9	ABX11396	Abx11396 Human pap
38	24.2	83.4	1518	9	ADA27368	Ada27368 HPV-16 L1
39	24.2	83.4	1518	9	ADA92546	Ada92546 HPV-16 L1
40	24.2	83.4	1518	9	ADA14295	Ada14295 HPV-16 L1
41	24.2	83.4	1518	9	AAD58576	Aad58576 HPV-16 L1
42	24.2	83.4	1518	10	ACC47502	Acc47502 HPV 16 L1
43	24.2	83.4	1518	10	ACC47504	Acc47504 HPV 16 L1
44	24.2	83.4	1518	12	ADF83436	Adf83436 Human pap
45	24.2	83.4	1518	12	ADF83440	Adf83440 Human pap

ALIGNMENTS

RESULT 1
ADQ27974
ID ADQ27974 standard; DNA; 29 BP.
XX
AC ADQ27974;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human papillomavirus genotype detection PCR primer #4.
XX
KW ss; primer; detection; diagnosis; amplification;
KW Human Papillomavirus genotype; cervical-neoplasia;
KW oncogenic high-risk group.
XX
OS Human papillomavirus.
XX
PN WO2004050917-A1.
XX
PD 17-JUN-2004.
XX
PF 28-NOV-2003; 2003WO-KR002608.
XX
PR 29-NOV-2002; 2002KR-00075370.
PR 31-JUL-2003; 2003KR-00053147.
XX
PA (ALBI-) ALBIOMED CO LTD.
XX
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;
XX
DR WPI; 2004-450746/42.
XX
PT New general primer or primer pair, useful for amplifying and detecting,
PT or for use in a nucleic acid amplification process for amplifying Human
PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT genotypes.
XX
PS Claim 1; SEQ ID NO 4; 71pp; English.
XX
CC The invention relates to a general primer or primer pair for amplifying
CC and detecting or for use in a nucleic acid amplification process for
CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC useful for amplifying cervical-neoplasia related HPV genotypes including

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CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 29 BP; 8 A; 1 C; 11 G; 9 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 12;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.0099;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||||||||||||||||
Db          1 GATGGTGATATGGTAGATACAGGATTTGG 29


RESULT 2
AAQ23183
ID   AAQ23183 standard; DNA; 38 BP.
XX
AC   AAQ23183;
XX
DT   06-AUG-1992  (first entry)
XX
DE   HPV probe 36.
XX
KW   Human papilloma virus; LCR; ligase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   EP477972-A.
XX
PD   01-APR-1992.
XX
PF   27-SEP-1991;   91EP-00116561.
XX
PR   28-SEP-1990;   90US-00589948.
PR   28-SEP-1990;   90US-00590105.
PR   28-SEP-1990;   90US-00590253.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Joseph JL,  Bouma SR,  Marshall RL,  Laffler TG;
XX
DR   WPI; 1992-106365/14.
XX
PT   Compsns. for amplifying DNA of human papilloma virus by LCR and PCR - and
PT   consensus and type specific oligo-nucleotide(s), for diagnosis of HPV-
PT   esp. types 6,11,16,18 33 and 61.
XX
PS   Claim 18 + Example 5; Page 69 + 11-13; 76pp; English.
XX
CC   Probe 36 maps to HPV types 6 (6365-6402), 11 (6350-6387), 16 (6225-6262),
CC   18 (6201-6238) and 33 (6182-6219). Sequences were selected according to
CC   an unique algorithm developed to choose consensus sequences. The
CC   sequences represented in AAQ23167-88 are consensus sequences selected so
CC   each should hybridise with each of human HPV types 6, 11, 16, 18 and 33.
CC   The sequences represented in AAQ23095-189 and AAQ25590 allow the
CC   detection of small amts. of HPV DNA, e.g. from cervical lesion samples,
CC   using PCR or LCR amplification procedures. The use of nucleic acids
CC   allows greater discrimination among viral subtypes than antibodies, and
CC   the use of DNA-based tests increases both the sensitivity and the
CC   specificity of prior-art antibody based tests. The oligonucleotides can
CC   be used either to detect specific sequences of specific HPV types, or
CC   consensus regions with homology among different types
XX
SQ   Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 2;  Length 38;
  Best Local Similarity   93.1%;  Pred. No. 0.25;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||| ||||||| |||||
Db          1 GATGGTGATATGGTTGATACAGGCTTTGG 29


RESULT 3
AAT29878
ID   AAT29878 standard; DNA; 38 BP.
XX
AC   AAT29878;
XX
DT   25-MAR-2003  (revised)
DT   19-JUL-1996  (first entry)
XX
DE   Human papillomavirus detection probe 36.
XX
KW   primer; probe; human papillomvirus; PCR; amplification; LCR; ligation;
KW   fluorescein; biotin; ss.
XX
OS   Synthetic.
XX
PN   US5484699-A.
XX
PD   16-JAN-1996.
XX
PF   30-SEP-1994;   94US-00316293.
XX
PR   28-SEP-1990;   90US-00589948.
PR   28-SEP-1990;   90US-00590105.
PR   28-SEP-1990;   90US-00590253.
PR   22-OCT-1992;   92US-00965665.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Marshall RL,  Bouma SR,  Laffler TG,  Joseph JL;
XX
DR   WPI; 1996-087060/09.
XX
PT   New human papilloma virus type-specific oligo:nucleotide(s) - used for
PT   the detection of and determination of the type of HPV in test samples.
XX
PS   Example 5; Col 13-14; 37pp; English.
XX
CC   The sequences AAT29826-T29921 represent primers and probes derived from
CC   human papillomvirus genomic sequences and are used to detect the presence
CC   of human papillomavirus types 6, 11, 16, 18, 31 and 33 in samples. The
CC   detection is either by PCR or LCR. Alternatively the sequences can be
CC   labelled with fluorescein or biotin and used as probes. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 2;  Length 38;
  Best Local Similarity   93.1%;  Pred. No. 0.25;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||| ||||||| |||||
Db          1 GATGGTGATATGGTTGATACAGGCTTTGG 29


RESULT 4
AAV15595
ID   AAV15595 standard; DNA; 386 BP.
XX
AC   AAV15595;
XX
DT   25-MAR-2003  (revised)
DT   30-JUL-1998  (first entry)
XX
DE   Papillomavirus major capsid protein DNA from plasmid DL20.
XX
```

```
KW   Major capsid protein; detection; infection; disease; wart; cancer; skin;
KW   diagnosis; treatment; prevention; vaccine; cervix; mouth; throat; ds.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .386
FT                   /*tag=  a
FT                   /product= "major capsid protein"
FT                   /note= "partial coding sequence"
XX
PN   DE19648962-C1.
XX
PD   26-FEB-1998.
XX
PF   26-NOV-1996;   96DE-01048962.
XX
PR   26-NOV-1996;   96DE-01048962.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   De Villiers- Zur Hausen E,  Zur Hausen H,  Lavergne D,  Benton C;
XX
DR   WPI; 1998-121621/12.
DR   P-PSDB; AAW47277.
XX
PT   DNA encoding peptide(s) from papilloma virus major capsid protein - and
PT   related proteins, vectors, transformed cells and antibodies, for
PT   diagnosis, treatment and prevention of papilloma virus infection and
PT   disease.
XX
PS   Claim 1; Fig 2; 16pp; German.
XX
CC   This sequence encodes a fragment of the human papillomavirus (PV) major
CC   capsid protein isolated from plasmid DL20. This fragment could be used as
CC   a reagent for detecting PV infections and diseases (e.g. warts or cancers
CC   of skin, cervix or mouth/throat, particularly of the skin). Cells
CC   containing transformants can be used to produce recombinant
CC   papillomavirus which can be used for diagnosis, treatment and prevention
CC   (as vaccines) of papillomavirus infection. (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 386 BP; 129 A; 62 C; 84 G; 111 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 2;  Length 386;
  Best Local Similarity   93.1%;  Pred. No. 0.34;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||||| | |||||||||
Db          7 GATGGTGATATGGTAGACATAGGATTTGG 35


RESULT 5
AAL47486
ID   AAL47486 standard; DNA; 1421 BP.
XX
AC   AAL47486;
XX
DT   13-SEP-2002  (first entry)
XX
DE   HPV type 18 L1 gene mutant L1deltaC*.
XX
KW   Human papillomavirus type 18; HPV; cancer; L protein; E protein;
KW   cytostatic; virucide; vaccine; lung; cervix; penis; vulva; anus; gene;
KW   ds.
XX
OS   Human papillomavirus type 18.
OS   Synthetic.
XX
PN   DE10059630-A1.
XX
PD   06-JUN-2002.
XX
PF   01-DEC-2000; 2000DE-01059630.
XX
PR   01-DEC-2000; 2000DE-01059630.
XX
PA   (MEDI-) MEDIGENE AG.
XX
PI   Mueller R,  Nieland J,  Gabelsberger J,  Herbst R;
XX
DR   WPI; 2002-520969/56.
DR   P-PSDB; AAO18098.
XX
PT   Composition for treating and preventing tumors caused by human papilloma
PT   virus 18, contains fusion protein of papilloma virus L and E proteins,
PT   preferably truncated.
XX
PS   Disclosure; Page 14-15; 64pp; German.
XX
CC   The present invention relates to a composition for preventing or treating
CC   tumours caused by human papillomavirus (HPV) 18, involving at least one
CC   fusion protein of at least one each of L and E proteins from one or more
CC   papillomaviruses, and optionally also additives or auxiliaries. The
CC   composition can be used as a vaccine to treat or prevent carcinoma of the
CC   lung, cervix, penis, vulva and anus. The present sequence is an HPV gene
XX
SQ   Sequence 1421 BP; 371 A; 260 C; 316 G; 474 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 6;  Length 1421;
  Best Local Similarity   93.1%;  Pred. No. 0.4;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||||| |||| |||
Db        589 GATGGTGATATGGTAGATACTGGATATGG 617


RESULT 6
AEA12674
ID   AEA12674 standard; DNA; 1497 BP.
XX
AC   AEA12674;
XX
DT   28-JUL-2005  (first entry)
XX
DE   DNA encoding human papillomavirus 58 L1 protein, 58 L1 wt sequence.
XX
KW   papillomavirus infection; uterine cervix tumor; carcinoma; HPV58 L1;
KW   virus-like particle; vaccine; expression; recombinant protein;
KW   transformation; immune stimulation; virucide; ds; gene.
XX
OS   Human papillomavirus - 58.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1497
FT                   /*tag=  a
FT                   /product= "HPV58 L1"
XX
PN   WO2005047315-A2.
XX
PD   26-MAY-2005.
XX
PF   10-NOV-2004; 2004WO-US037372.
XX
PR   12-NOV-2003; 2003US-0519211P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Bryan JT,  Brownlow MK,  Schultz LD,  Wang X,  Jansen KU;
XX
DR   WPI; 2005-372343/38.
DR   P-PSDB; AEA12673.
XX
PT   New nucleic acid molecule encoding HPV58 L1, useful for immunoprophylaxis
```

PT against papillomavirus infection, and for treating existing human
PT papillomavirus infection.
XX
PS Disclosure; SEQ ID NO 3; 39pp; English.
XX
CC The new invention relates to the prevention and therapy of human
CC papillomavirus (HPV) infection. More than 90% of cervical carcinomas are
CC associated with infections of HPV31, HPV-33, -45, -52, and -58. The L1
CC protein is the major capsid protein and is highly conserved among
CC different papillomaviruses. Expression of the L1 and L2 proteins in
CC yeast, insect, mammal or bacterial cells leads to self-assembly of virus-
CC like particles (VLPs). VPLs are similar to authentic virions and are
CC capable of inducing high titres of neutralizing antibodies when
CC administered into animals, without the potentially oncogenic viral
CC genome. Therefore, L1 and L2 genes have been identified as immunological
CC targets for the development of prophylactic and therapeutic vaccines for
CC HPV infection. Vaccine development has been limited by difficulties in
CC obtaining high expression levels of capsid proteins. The present
CC invention provides a nucleic acid (SEQ ID NO:1) encoding HPV58 L1 protein
CC (SEQ ID No: 2), which is codon-optimized for high-level expression in
CC yeast cells. Virus-like particles (VLPs) are also disclosed comprised of
CC recombinant L1 protein or recombinant L1 + L2 proteins of HPV58.
CC Described is a method of producing the VLPs by transforming yeast with
CC the HPV58 L1 gene, and cultivating the yeast under conditions that permit
CC expression of the protein. Specifically claimed is a vaccine comprising
CC the VLPs. The gene and vaccine are useful for immunoprophylaxis against
CC papillomavirus infection, and for treating existing human papillomavirus
CC infection. The present sequence is DNA encoding human papillomavirus 58
CC L1 protein, designated 58 L1 wt.
XX
SQ Sequence 1497 BP; 445 A; 280 C; 310 G; 462 T; 0 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 14; Length 1497;
Best Local Similarity 93.1%; Pred. No. 0.4;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||| ||||||||||||||| |||||
Db 589 GATGGTGACATGGTAGATACAGGGTTTGG 617

RESULT 7
AAT40119
ID AAT40119 standard; DNA; 1524 BP.
XX
AC AAT40119;
XX
DT 28-JAN-1997 (first entry)
XX
DE Human papillomavirus type 18 L1 capsid protein gene.
XX
KW HPV-18; L1 gene; capsid protein; vaccine; diagnosis; vector; antibody;
KW serotyping; cervix carcinoma; ss.
XX
OS Human papillomavirus type 18.
XX
PN WO9629413-A2.
XX
PD 26-SEP-1996.
XX
PF 18-MAR-1996; 96WO-US003649.
XX
PR 22-MAR-1995; 95US-00408669.
PR 22-MAR-1995; 95US-00409122.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hofmann KJ, Jansen KU, Neeper MP, Joyce JG, George HA;
XX
DR WPI; 1996-443188/44.
DR P-PSDB; AAW05843.
XX
PT DNA encoding human papilloma virus 18, esp. L1 and L2 capsid proteins -
PT and related vectors and antibodies, useful in protective vaccines, for
PT serotyping HPV infections and as therapeutic agents.
XX
PS Claim 2; Fig 1; 46pp; English.
XX
CC The L1 gene (AAT40119) codes for the major capsid protein (AAW05843) of
CC human papillomavirus type 18 (HPV18), an HPV type associated with
CC invasive carcinomas of the cervix, vagina, vulva and anal canal. The DNA
CC sequence was deduced from a genomic clone isolated from human cervical
CC carcinoma-derived SW756 cells using an HPV18 L1 probe. The HPV18 L1 and
CC L2 (see also AAT40120) genes can be used in vaccines against HPV18
CC infection, as probes, or to produce recombinant capsid proteins in host
CC cells
XX
SQ Sequence 1524 BP; 396 A; 292 C; 337 G; 499 T; 0 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 2; Length 1524;
Best Local Similarity 93.1%; Pred. No. 0.4;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||||||||| |||| |||
Db 589 GATGGTGATATGGTAGATACTGGATATGG 617

RESULT 8
AAQ04472
ID AAQ04472 standard; DNA; 1950 BP.
XX
AC AAQ04472;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 04-OCT-1990 (first entry)
XX
DE Human papilloma virus 52 clone pCD15 noncoding region.
XX
KW Human papilloma virus type 52; HPV infection; probes; cervical cancer;
KW ss.
XX
OS Human papillomavirus type 52.
XX
PN EP370625-A.
XX
PD 30-MAY-1990.
XX
PF 24-OCT-1989; 89EP-00310934.
XX
PR 26-OCT-1988; 88US-00262597.
XX
PA (GEOU) UNIV GEORGETOWN.
XX
PI Lancaster WD;
XX
DR WPI; 1990-165336/22.
XX
PT Human papilloma-virus type 52 DNA and RNA - used in probes for detecting
PT HPV infection in samples and for blocking HPV gene expression.
XX
PS Disclosure; Page ?; -pp; English.
XX
CC This partial sequence is from the middle of the L1 ORF through the
CC noncoding region. Comparison of the sequence of HPV33 and HPV 52 revealed
CC 75% homology in the L1ORF and less than 50% homology in the noncoding
CC region. The HPV 52 was isolated and cloned from the combined DNA of
CC biopsies of 2 mild dysplasias. The DNA was cloned into lambda L47 and
CC positive plaques by nonstringent hybridisation with HPV-16 probes were
CC isolated to obtain HPV 52 DNA. The probes obtained from this sequence can
CC be used for detecting HPV infection in a sample, for assessing the risk
CC of cancer development, in partic. for detecting HPV 52 which may play a
CC role in cervical cancer development. The HPV 52 anti-sense RNA or
CC fragments can be used as blockers or regulators of HPV gene expression in
CC general and HPV 52 in partic. (Updated on 25-MAR-2003 to correct PA

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CC   field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 1950 BP; 551 A; 376 C; 380 G; 643 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 2;  Length 1950;
  Best Local Similarity   93.1%;  Pred. No. 0.42;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||| || ||||||||||||||||||||||
Db        138 GATGGGGACATGGTAGATACAGGATTTGG 166


RESULT 9
AAN91804
ID   AAN91804 standard; DNA; 2017 BP.
XX
AC   AAN91804;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   16-MAR-1990  (first entry)
XX
DE   Human papilloma virus type 33 marker fragment.
XX
KW   Cervical cancer.
XX
OS   Human papillomavirus type 33.
XX
PN   WO8909940-A.
XX
PD   19-OCT-1989.
XX
PF   04-APR-1989;   89WO-US001318.
XX
PR   04-APR-1988;   88US-00177404.
PR   31-MAR-1989;   89US-00330381.
XX
PA   (ONCO-) ONCOR INC.
XX
PI   George AL,  Groff DE;
XX
DR   WPI; 1989-324314/44.
XX
PT   Rapid detection of specific human papilloma virus genotypes - by
PT   hybridisation of DNA digest with new labelled nucleic acid probes.
XX
PS   Disclosure; Fig 23; 81pp; English.
XX
CC   Used as a probe. The patent describes probes (DNA or RNA) and their
CC   complements capable of detecting one or a combination of HPV types 6, 11,
CC   16, 18, 31, 33 and 35. (Updated on 25-MAR-2003 to correct PR field.)
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 2017 BP; 583 A; 399 C; 373 G; 662 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 1;  Length 2017;
  Best Local Similarity   93.1%;  Pred. No. 0.42;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||| || ||||||||||
Db       1453 GATGGTGATATGGTGGACACAGGATTTGG 1481


RESULT 10
ADZ45651
ID   ADZ45651 standard; DNA; 7824 BP.
XX
AC   ADZ45651;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Human papillomavirus type 58 full length genomic clone - SEQ ID 5.
XX
KW   tumor marker; genome; diagnosis; cancer; uterine cervix tumor;
KW   rectal tumor; colon tumor; ds.
XX
OS   Human papillomavirus type 58.
XX
PN   WO2005033333-A2.
XX
PD   14-APR-2005.
XX
PF   04-OCT-2004; 2004WO-DK000670.
XX
PR   07-OCT-2003; 2003DK-00001474.
PR   07-OCT-2003; 2003US-0509205P.
PR   13-FEB-2004; 2004US-0543925P.
XX
PA   (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
PI   Chau MF,  Bisgaard-Franzen K,  Lin J,  Rasmussen OF,  Wang Z,  Lusk J;
PI   Lindberg M,  Yoast S;
XX
DR   WPI; 2005-285441/29.
XX
PT   New composition having a nucleic acid molecule identical to genomic clone
PT   of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT   risk of developing cancer, in particular cervical, anal, colon and HPV-
PT   related cancer.
XX
PS   Claim 2; SEQ ID NO 5; 169pp; English.
XX
CC   The invention comprises a composition for the detection of cancer
CC   markers, the composition contains a nucleic acid molecule which is
CC   substantially identical to a full length genomic clone of a human
CC   papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
CC   composition of the invention is useful for diagnosing cancer or the risk
CC   of developing cancer, in particular cervical, anal, colon and HPV-related
CC   cancer. The present DNA sequence represents a human papilloma virus full
CC   length genomic clone of the invention.
XX
SQ   Sequence 7824 BP; 2487 A; 1388 C; 1576 G; 2373 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 14;  Length 7824;
  Best Local Similarity   93.1%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||| ||||||||||||||| |||||
Db       6231 GATGGTGACATGGTAGATACAGGGTTTGG 6259


RESULT 11
ADZ45648
ID   ADZ45648 standard; DNA; 7857 BP.
XX
AC   ADZ45648;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Human papillomavirus type 18 full length genomic clone - SEQ ID 2.
XX
KW   tumor marker; genome; diagnosis; cancer; uterine cervix tumor;
KW   rectal tumor; colon tumor; ds.
XX
OS   Human papillomavirus type 18.
XX
PN   WO2005033333-A2.
XX
PD   14-APR-2005.
XX
PF   04-OCT-2004; 2004WO-DK000670.
XX
PR   07-OCT-2003; 2003DK-00001474.
```

PR 07-OCT-2003; 2003US-0509205P.
PR 13-FEB-2004; 2004US-0543925P.
XX
PA (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
PI Chau MF, Bisgaard-Franzen K, Lin J, Rasmussen OF, Wang Z, Lusk J;
PI Lindberg M, Yoast S;
XX
DR WPI; 2005-285441/29.
XX
PT New composition having a nucleic acid molecule identical to genomic clone
PT of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT risk of developing cancer, in particular cervical, anal, colon and HPV-
PT related cancer.
XX
PS Claim 1; SEQ ID NO 2; 169pp; English.
XX
CC The invention comprises a composition for the detection of cancer
CC markers, the composition contains a nucleic acid molecule which is
CC substantially identical to a full length genomic clone of a human
CC papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
CC composition of the invention is useful for diagnosing cancer or the risk
CC of developing cancer, in particular cervical, anal, colon and HPV-related
CC cancer. The present DNA sequence represents a human papilloma virus full
CC length genomic clone of the invention.
XX
SQ Sequence 7857 BP; 2365 A; 1497 C; 1680 G; 2315 T; 0 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 14; Length 7857;
Best Local Similarity 93.1%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||||||||| |||| |||
Db 6201 GATGGTGATATGGTAGATACTGGATATGG 6229

RESULT 12
ADN12113
ID ADN12113 standard; DNA; 7880 BP.
XX
AC ADN12113;
XX
DT 17-JUN-2004 (first entry)
XX
DE HPV type 13 genome #1.
XX
KW major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
KW EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma;
KW gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma;
KW parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
XX
OS Human Papilloma Virus.
XX
PN WO2004027036-A2.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029684.
XX
PR 19-SEP-2002; 2002US-0411990P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Ambinder RF, Yang Y, Borrello IM, Levitsky HI;
XX
DR WPI; 2004-295406/27.
XX
PT New human cell line modified to comprise and express genes encoding
PT immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for
PT inducing or stimulating an immune response in a human to EBV-associated
PT cancer.
XX
PS Example 1; SEQ ID NO 6; 218pp; English.
XX
CC The present invention relates to a human cell line, which lacks major
CC histocompatibility class I(MHC-I) and MHC-II antigens and which has been
CC modified to comprise and express a gene encoding an immunomodulator and a
CC gene encoding an antigen of Epstein-Barr virus (EBV). The human cell
CC line, compositions and methods are useful for inducing or stimulating an
CC immune response in a human to an EBV-associated cancer, where the human
CC has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma,
CC gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma,
CC parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present
CC sequence represents a nucleotide sequence associated with the cell line
CC of the invention.
XX
SQ Sequence 7880 BP; 2452 A; 1480 C; 1628 G; 2320 T; 0 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 12; Length 7880;
Best Local Similarity 93.1%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||||||||| |||| |||
Db 6321 GATGGTGACATGGTGGATACAGGATTTGG 6349

RESULT 13
ADN12111
ID ADN12111 standard; DNA; 7896 BP.
XX
AC ADN12111;
XX
DT 17-JUN-2004 (first entry)
XX
DE HPV type 59 genome #1.
XX
KW major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
KW EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma;
KW gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma;
KW parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
XX
OS Human Papilloma Virus.
XX
PN WO2004027036-A2.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029684.
XX
PR 19-SEP-2002; 2002US-0411990P.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Ambinder RF, Yang Y, Borrello IM, Levitsky HI;
XX
DR WPI; 2004-295406/27.
XX
PT New human cell line modified to comprise and express genes encoding
PT immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for
PT inducing or stimulating an immune response in a human to EBV-associated
PT cancer.
XX
PS Example 1; SEQ ID NO 4; 218pp; English.
XX
CC The present invention relates to a human cell line, which lacks major
CC histocompatibility class I(MHC-I) and MHC-II antigens and which has been
CC modified to comprise and express a gene encoding an immunomodulator and a
CC gene encoding an antigen of Epstein-Barr virus (EBV). The human cell
CC line, compositions and methods are useful for inducing or stimulating an
CC immune response in a human to an EBV-associated cancer, where the human
CC has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma,
CC gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma,
CC parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present
CC sequence represents a nucleotide sequence associated with the cell line

```
CC   of the invention.
XX
SQ   Sequence 7896 BP; 2473 A; 1457 C; 1594 G; 2372 T; 0 U; 0 Other;

  Query Match             89.0%;  Score 25.8;  DB 12;  Length 7896;
  Best Local Similarity   93.1%;  Pred. No. 0.5;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||||| ||||||| |||
Db       6194 GATGGTGATATGGTAGACACAGGATATGG 6222


RESULT 14
AAT47256
ID   AAT47256 standard; DNA; 410 BP.
XX
AC   AAT47256;
XX
DT   05-SEP-1997  (first entry)
XX
DE   (DSM 10097) human papillomavirus major capsid protein DNA.
XX
KW   HPV; major; capsid; L1; HPV48; pVS201-1; DSM 10097; diagnosis; disease;
KW   skin cancer; therapy; prevention; vaccination; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1. .408
FT                   /*tag=  a
FT                   /label= major_capsid_protein
XX
PN   DE19526386-C1.
XX
PD   02-JAN-1997.
XX
PF   19-JUL-1995;   95DE-01026386.
XX
PR   19-JUL-1995;   95DE-01026386.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Shamanin V,  Villiers-Zur Hausen E,  Zur Hausen H;
XX
DR   WPI; 1997-043923/05.
DR   P-PSDB; AAW07854.
XX
PT   DNA encoding peptide(s) of papilloma major capsid protein - useful for
PT   diagnosis, treatment and prevention of papilloma virus disease.
XX
PS   Claim 1; Fig 3; 15pp; German.
XX
CC   The present sequence, which encodes a human papillomavirus (HPV) major
CC   capsid (L1) protein, is 69.4% homologous to the HPV48 L1 DNA. The
CC   encoding DNA, which is contained in pVS201-1 (DSM 10097), is useful for
CC   the diagnosis of HPV diseases, especially skin cancer, and for the
CC   preparation of the protein. The protein is useful for the diagnosis,
CC   therapy and prevention (by vaccination) of these diseases
XX
SQ   Sequence 410 BP; 116 A; 69 C; 99 G; 126 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 1.7;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||  |||| |||||||||
Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 15
ADF89368
ID   ADF89368 standard; DNA; 1422 BP.
XX
AC   ADF89368;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Plant-optimised NLS-deleted Human papillomavirus type 16 L1 DNA.
XX
KW   papillomavirus virus-like particle; capsomere; transgenic; plant;
KW   L1 capsid; gene therapy; HPV16; ds; gene; mutant.
XX
OS   Synthetic.
OS   Human papillomavirus type 16.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1422
FT                   /*tag=  a
FT                   /product= "Plant-optimised NLS-deleted Human
FT                   papillomavirus type 16 L1 protein"
XX
PN   WO2003093437-A2.
XX
PD   13-NOV-2003.
XX
PF   02-MAY-2003; 2003WO-US013757.
XX
PR   02-MAY-2002; 2002US-0377467P.
XX
PA   (UYRP ) UNIV ROCHESTER.
PA   (BOYC-) BOYCE THOMPSON INST PLANT RES INC.
XX
PI   Rose RC,  Mason HS,  Warzecha H;
XX
DR   WPI; 2004-011891/01.
DR   P-PSDB; ADF89369.
XX
PT   Producing papillomavirus virus-like particles or capsomeres comprises
PT   providing a transgenic plant or plant seed transformed with a nucleic
PT   acid molecule comprising a papillomavirus L1 capsid protein coding
PT   sequences.
XX
PS   Example 9; SEQ ID NO 8; 74pp; English.
XX
CC   The invention relates to a novel method for producing papillomavirus
CC   virus-like particles or capsomeres comprising providing a transgenic
CC   plant or plant seed transformed with a nucleic acid molecule comprising
CC   papillomavirus L1 capsid protein coding sequences and growing the
CC   transgenic plant or transgenic plant grown from the transgenic plant seed
CC   under conditions effective to produce the virus-like particles containing
CC   the papillomavirus L1 capsid protein. The invention may have virucide
CC   applications whilst the methods, genetic construct and plant may be
CC   useful for immunising a subject against a disease resulting from
CC   infection by a papillomavirus, as well as during gene therapy procedures.
CC   The current sequence is that of the plant-optimised NLS (nuclear
CC   localisation signal)-deleted Human papillomavirus type 16 (HPV16) L1 DNA
CC   of the invention.
XX
SQ   Sequence 1422 BP; 384 A; 343 C; 296 G; 399 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 12;  Length 1422;
  Best Local Similarity   89.7%;  Pred. No. 1.9;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTGGATACTGGCTTTGG 617


Search completed: March  5, 2006, 22:12:07
Job time : 383.5 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:59:29 ; Search time 3168 Seconds
(without alignments)
428.291 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		21.2	73.1	601	3	BI505309	BI505309 BB170020B
2		21	72.4	687	10	CW611284	CW611284 OA_ABa015
3		21	72.4	738	10	AG537642	AG537642 Mus muscu
4		21	72.4	810	10	CZ694085	CZ694085 OC__Ba000
5		20.6	71.0	358	1	AL836877	AL836877 AL836877
6		20.6	71.0	370	1	AL836861	AL836861 AL836861
7	c	20.6	71.0	465	9	AZ159603	AZ159603 SP_0064_A
8		20.6	71.0	605	11	FR0037014	AL124517 Fugu rubr
9	c	20.6	71.0	770	3	BJ148396	BJ148396 BJ148396
10		20.6	71.0	776	2	BE277163	BE277163 601178502
11	c	20.4	70.3	250	1	AI020455	AI020455 ub26g05.r
12	c	20.4	70.3	327	1	AA210582	AA210582 mu71a03.r
13		20.4	70.3	490	2	BF147434	BF147434 us31g01.x
14	c	20.4	70.3	528	5	BX513029	BX513029 BX513029
15	c	20.2	69.7	1020	10	CL056918	CL056918 CH216-83P
16		20	69.0	137	9	AZ693668	AZ693668 AST-2HLB5
17	c	20	69.0	215	1	AW273632	AW273632 xv67h03.x
18	c	20	69.0	219	8	F04754	F04754 HSCZWG022 n
19		20	69.0	258	1	AW900192	AW900192 CM0-NN100
20	c	20	69.0	282	8	Z39966	Z39966 HSC1NH042 n
21	c	20	69.0	325	7	CV376112	CV376112 PM3-SN001
22	c	20	69.0	353	1	AW207569	AW207569 UI-H-BI1-
23		20	69.0	353	9	AQ357418	AQ357418 CITBI-E1-
24		20	69.0	356	5	BX115022	BX115022 BX115022
25		20	69.0	371	1	AI609876	AI609876 tt83e01.x
26		20	69.0	380	6	CF017665	CF017665 QBM2b09.x
27		20	69.0	380	6	CF017813	CF017813 QBM4a04.x
28		20	69.0	394	1	AA578113	AA578113 nl29a01.s
29		20	69.0	430	9	AQ093787	AQ093787 HS_3023_B
30		20	69.0	443	9	AQ334764	AQ334764 HS_5009_B
31		20	69.0	489	9	AQ357438	AQ357438 CITBI-E1-
32		20	69.0	510	9	CE148431	CE148431 tigr-gss-
33		20	69.0	526	6	CD307313	CD307313 StrPu691.
34		20	69.0	562	2	BF970237	BF970237 602273477
35	c	20	69.0	614	8	DN485400	DN485400 N001G08.3
36		20	69.0	703	5	BU685954	BU685954 UI-CF-DU1
37	c	20	69.0	746	7	CK351524	CK351524 hggfha39D
38		20	69.0	747	2	BE730479	BE730479 601562994
39		20	69.0	811	10	CW750547	CW750547 OP__Ba006
40	c	20	69.0	834	7	CO087160	CO087160 GR__Ea05H
41		20	69.0	888	3	BQ223384	BQ223384 AGENCOURT
42		20	69.0	1494	4	AK042726	AK042726 Mus muscu
43	c	19.8	68.3	554	9	CE113095	CE113095 tigr-gss-
44		19.8	68.3	649	8	DR532869	DR532869 WS02739.C
45	c	19.8	68.3	786	10	DU075702	DU075702 80192 Tom

ALIGNMENTS

RESULT 1
BI505309
LOCUS BI505309 601 bp mRNA linear EST 08-APR-2002
DEFINITION BB170020B10F08.5 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170020B10F08 5', mRNA sequence.
ACCESSION BI505309
VERSION BI505309.1 GI:15355683
KEYWORDS EST.
SOURCE Apis mellifera (honey bee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
REFERENCE 1 (bases 1 to 601)
AUTHORS Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
TITLE Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
JOURNAL Genome Res. 12 (4), 555-566 (2002)
PUBMED 11932240
COMMENT Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobi@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR PRimers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Plate: BB170020B10 row: F column: 08
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 601.
FEATURES Location/Qualifiers
source 1. .601
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB170020B10F08"

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                     /sex="female"
                     /tissue_type="brain"
                     /dev_stage="adult worker honey bee"
                     /lab_host="DH10B"
                     /clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
                     /note="Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1;
                     Site_2: Not1; This BB17 cDNA library was generated by
                     subtraction of the BB16  library with 4000 previously
                     sequenced clones. The BB16 library was  contributed by the
                     Soares laboratory and it was constructed and  normalized
                     as described by Bonaldo, M.F., Lennon, G. and  Soares,
                     M.B. (1996), Genome Research 6(9): 791-806. RNA was
                     prepared  from dissected brains of adult worker bees of
                     various ages and  various behavioral groups. "
ORIGIN

  Query Match             73.1%;  Score 21.2;  DB 3;  Length 601;
  Best Local Similarity   88.5%;  Pred. No. 2.6e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATT 26
              ||||||||| | | ||||||||||||
Db         98 GATGGTGATCTTGGAGATACAGGATT 123


RESULT 2
CW611284
LOCUS       CW611284                687 bp    DNA     linear   GSS 22-OCT-2004
DEFINITION  OA_ABa0153A01.r OA_ABa Oryza australiensis genomic clone
            OA_ABa0153A01 3', genomic survey sequence.
ACCESSION   CW611284
VERSION     CW611284.1  GI:54528096
KEYWORDS    GSS.
SOURCE      Oryza australiensis
  ORGANISM  Oryza australiensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 687)
  AUTHORS   Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
            Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
  TITLE     OMAP Project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0153  row: A  column: 01
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .687
                     /organism="Oryza australiensis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4532"
                     /clone="OA_ABa0153A01"
                     /tissue_type="young leaves"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OA_ABa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             72.4%;  Score 21;  DB 10;  Length 687;
  Best Local Similarity   82.8%;  Pred. No. 3.3e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||| |||||||||||| | |||||  ||
Db        350 GATGGAGATATGGTAGAAAGAGGATGAGG 378


RESULT 3
AG537642
LOCUS       AG537642                738 bp    DNA     linear   GSS 23-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-449L22.T7, genomic survey
            sequence.
ACCESSION   AG537642
VERSION     AG537642.1  GI:48298056
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
   PUBMED   15574823
REFERENCE   2  (bases 1 to 738)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector     : pBACe3.6
            R.Site 1   : EcoRI
            R.Site 2   : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .738
                     /organism="Mus musculus molossinus"
                     /mol_type="genomic DNA"
                     /sub_species="molossinus"
                     /db_xref="taxon:57486"
                     /clone="MSMg01-449L22.T7"
                     /sex="male"
                     /tissue_type="mixture of kidney and spleen"
                     /clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN

  Query Match             72.4%;  Score 21;  DB 10;  Length 738;
  Best Local Similarity   82.8%;  Pred. No. 3.3e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||| ||| |||||||||||||| | | ||
Db        649 GATGCTGACATGGTAGATACAGCAGTGGG 677


RESULT 4
CZ694085
LOCUS       CZ694085                810 bp    DNA     linear   GSS 25-JUL-2005
DEFINITION  OC__Ba0006L20.r OC__Ba Oryza coarctata genomic clone OC__Ba0006L20
            3', genomic survey sequence.
```

```
ACCESSION   CZ694085
VERSION     CZ694085.1  GI:71093233
KEYWORDS    GSS.
SOURCE      Oryza coarctata (Porteresia coarctata)
  ORGANISM  Oryza coarctata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 810)
  AUTHORS   Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wing,R.
  TITLE     OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR PRimers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0006  row: L  column: 20
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .810
                     /organism="Oryza coarctata"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:77588"
                     /clone="OC__Ba0006L20"
                     /tissue_type="leaves"
                     /dev_stage="mature"
                     /lab_host="DH10B"
                     /clone_lib="OC__Ba"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
ORIGIN

  Query Match             72.4%;  Score 21;  DB 10;  Length 810;
  Best Local Similarity   82.8%;  Pred. No. 3.3e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||| |||||  |||| || |||||||
Db        234 GATGGTAATATGCAAGATGCATGATTTGG 262


RESULT 5
AL836877
LOCUS       AL836877                358 bp    mRNA    linear   EST 27-FEB-2004
DEFINITION  AL836877 EFRe Takifugu rubripes cDNA clone EFRe040apcK8, mRNA
            sequence.
ACCESSION   AL836877
VERSION     AL836877.1  GI:21878839
KEYWORDS    EST.
SOURCE      Takifugu rubripes (Fugu rubripes)
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Clark,M.S., Edwards,Y.J., Peterson,D., Clifton,S.W., Thompson,A.J.,
            Sasaki,M., Suzuki,Y., Kikuchi,K., Watabe,S., Kawakami,K.,
            Sugano,S., Elgar,G. and Johnson,S.L.
  TITLE     Fugu ESTs: new resources for transcription analysis and genome
            annotation
  JOURNAL   Genome Res. 13 (12), 2747-2753 (2003)
COMMENT     Contact: Clark MS
            MRC Human Genome Mapping Project Resource Centre
            Hinxton, Cambridge, CB10 1SB, UK
            Email: biohelp@hgmp.mrc.ac.uk
            Email: biohelp@hgmp.mrc.ac.uk
            Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            The clone can be obtained from www.hgmp.mrc.ac.uk
            Library created by Greg Elgar
            MRC Human Genome Mapping Project Resource Centre, Hinxton,
            Cambridge, CB10 1SB. UK
            Library sequenced by Sarah Warner and Jim Hills
            MRC Human Genome Mapping Project Resource Centre, Hinxton,
            Cambridge, CB10 1SB. UK.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Takifugu rubripes"
                     /mol_type="mRNA"
                     /db_xref="taxon:31033"
                     /clone="EFRe040apcK8"
                     /tissue_type="gonad"
                     /clone_lib="EFRe"
                     /note="Vector: pBluescript II KS"
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 1;  Length 358;
  Best Local Similarity   85.2%;  Pred. No. 4.5e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTT 27
              ||||||||| |||| ||  ||||||||
Db        222 GATGGTGATCTGGTGGACGCAGGATTT 248


RESULT 6
AL836861
LOCUS       AL836861                370 bp    mRNA    linear   EST 27-FEB-2004
DEFINITION  AL836861 EFRe Takifugu rubripes cDNA clone EFRe040apcK1, mRNA
            sequence.
ACCESSION   AL836861
VERSION     AL836861.1  GI:21878823
KEYWORDS    EST.
SOURCE      Takifugu rubripes (Fugu rubripes)
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Takifugu.
REFERENCE   1  (bases 1 to 370)
  AUTHORS   Clark,M.S., Edwards,Y.J., Peterson,D., Clifton,S.W., Thompson,A.J.,
            Sasaki,M., Suzuki,Y., Kikuchi,K., Watabe,S., Kawakami,K.,
            Sugano,S., Elgar,G. and Johnson,S.L.
  TITLE     Fugu ESTs: new resources for transcription analysis and genome
            annotation
  JOURNAL   Genome Res. 13 (12), 2747-2753 (2003)
COMMENT     Contact: Clark MS
            MRC Human Genome Mapping Project Resource Centre
            Hinxton, Cambridge, CB10 1SB, UK
            Email: biohelp@hgmp.mrc.ac.uk
            Email: biohelp@hgmp.mrc.ac.uk
            Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            The clone can be obtained from www.hgmp.mrc.ac.uk
            Library created by Greg Elgar
            MRC Human Genome Mapping Project Resource Centre, Hinxton,
            Cambridge, CB10 1SB. UK
            Library sequenced by Sarah Warner and Jim Hills
            MRC Human Genome Mapping Project Resource Centre, Hinxton,
            Cambridge, CB10 1SB. UK.
FEATURES             Location/Qualifiers
     source          1. .370
                     /organism="Takifugu rubripes"
                     /mol_type="mRNA"
                     /db_xref="taxon:31033"
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                     /clone="EFRe040apcK1"
                     /tissue_type="gonad"
                     /clone_lib="EFRe"
                     /note="Vector: pBluescript II KS"
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 1;  Length 370;
  Best Local Similarity   85.2%;  Pred. No. 4.5e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTT 27
              ||||||||| |||| ||  ||||||||
Db        205 GATGGTGATCTGGTGGACGCAGGATTT 231


RESULT 7
AZ159603/c
LOCUS       AZ159603                 465 bp    DNA     linear   GSS 29-AUG-2000
DEFINITION  SP_0064_A2_E10_T7A Strongylocentrotus purpuratus, purple sea
            urchin, sperm genomic BAC library Strongylocentrotus purpuratus
            genomic clone Plate=64 Col=20 Row=I, genomic survey sequence.
ACCESSION   AZ159603
VERSION     AZ159603.1  GI:8312225
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 465)
  AUTHORS   Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
            Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H.
            and Hood,L.
  TITLE     A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
   PUBMED   10920195
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 64  row: I  column: 20
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 465.
FEATURES             Location/Qualifiers
     source          1. .465
                     /organism="Strongylocentrotus purpuratus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7668"
                     /clone="Plate=64 Col=20 Row=I"
                     /clone_lib="Strongylocentrotus purpuratus, purple sea
                     urchin, sperm genomic BAC library"
                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                     DH10B"
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 9;  Length 465;
  Best Local Similarity   82.1%;  Pred. No. 4.6e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTG 28
              || |||||||||| || || || ||||||
Db         56 GAGGGTGATATGATANATTCATGATTTG 29


RESULT 8
FR0037014
LOCUS       FR0037014                605 bp    DNA     linear   GSS 25-FEB-2004
DEFINITION  Fugu rubripes GSS sequence, clone 045I08bB5, genomic survey
            sequence.
ACCESSION   AL124517
VERSION     AL124517.1  GI:6106132
KEYWORDS    GSS; genome survey sequence.
SOURCE      Takifugu rubripes (Fugu rubripes)
  ORGANISM  Takifugu rubripes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Takifugu.
REFERENCE   1
  AUTHORS   Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
            Bouchireb,N., Cottage,A., Yeo,G.S., Umrania,Y., Williams,G. and
            Brenner,S.
  TITLE     Generation and analysis of 25 Mb of genomic DNA from the pufferfish
            Fugu rubripes by sequence scanning
  JOURNAL   Genome Res. 9 (10), 960-971 (1999)
   PUBMED   10523524
REFERENCE   2  (bases 1 to 605)
  AUTHORS   Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,
            Umrania,Y., Williams,G. and Brenner,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
            Centre, Hinxton, Cambridge, CB10 1SB. UK Email:
            biohelp@hgmp.mrc.ac.uk
COMMENT     Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.
FEATURES             Location/Qualifiers
     source          1. .605
                     /organism="Takifugu rubripes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:31033"
                     /clone="045I08bB5"
                     /clone_lib="cosmid 045I08"
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 11;  Length 605;
  Best Local Similarity   85.2%;  Pred. No. 4.8e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTT 27
              ||||||||| |||| ||  ||||||||
Db         49 GATGGTGATCTGGTGGACGCAGGATTT 75


RESULT 9
BJ148396/c
LOCUS       BJ148396                 770 bp    mRNA    linear   EST 24-JAN-2002
DEFINITION  BJ148396 unpublished oligo-capped cDNA library, C. elegans L1 stage
            Caenorhabditis elegans cDNA clone yk1262d04 3', mRNA sequence.
ACCESSION   BJ148396
VERSION     BJ148396.1  GI:18316381
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
            and Sugano,S.
  TITLE     A complementary view of the C.elegans genome
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
```

```
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Caenorhabditis elegans"
                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /clone="yk1262d04"
                     /sex="hermaphrodite"
                     /tissue_type="whole animal"
                     /dev_stage="L1"
                     /clone_lib="unpublished oligo-capped cDNA library, C.
                     elegans L1 stage"
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 3;  Length 770;
  Best Local Similarity   85.2%;  Pred. No. 4.9e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGGATTTG 28
              |||| |||||||||||| | |||| |||
Db        558 ATGGGGATATGGTAGACAAAGGACTTG 532


RESULT 10
BE277163
LOCUS       BE277163                776 bp    mRNA    linear   EST 13-JUL-2000
DEFINITION  601178502F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3050832 5',
            mRNA sequence.
ACCESSION   BE277163
VERSION     BE277163.1  GI:9152129
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM97  row: d  column: 01
            High quality sequence stop: 754.
FEATURES             Location/Qualifiers
     source          1. .776
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3050832"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_20"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             71.0%;  Score 20.6;  DB 2;  Length 776;
  Best Local Similarity   85.2%;  Pred. No. 4.9e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 TGGTGATATGGTAGATACAGGATTTGG 29
              ||||| | | ||||| ||||||||||||
Db        529 TGGTGTTTTAGTAGAGACAGGATTTGG 555


RESULT 11
AI020455/c
LOCUS       AI020455                250 bp    mRNA    linear   EST 16-JUN-1998
DEFINITION  ub26g05.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1378904 5', mRNA sequence.
ACCESSION   AI020455
VERSION     AI020455.1  GI:3234791
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901372
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 234.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1378904"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares_thymus_2NbMT"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             70.3%;  Score 20.4;  DB 1;  Length 250;
  Best Local Similarity   95.5%;  Pred. No. 5.2e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGG 23
              ||||||||| ||||||||||||
Db         96 ATGGTGATAGGGTAGATACAGG 75


RESULT 12
```

```
AA210582/c
LOCUS       AA210582                327 bp    mRNA    linear   EST 29-JAN-1997
DEFINITION  mu71a03.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
            IMAGE:644812 5', mRNA sequence.
ACCESSION   AA210582
VERSION     AA210582.1  GI:1807829
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 327)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:396804
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 314.
FEATURES             Location/Qualifiers
     source          1. .327
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:644812"
                     /sex="male"
                     /tissue_type="lymph node"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse lymph node NbMLN"
                     /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGATACTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library constructed and
                     normalized by Bento Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             70.3%;  Score 20.4;  DB 1;  Length 327;
  Best Local Similarity   95.5%;  Pred. No. 5.4e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGG 23
              ||||||||| ||||||||||||
Db        126 ATGGTGATAGGGTAGATACAGG 105


RESULT 13
BF147434
LOCUS       BF147434                490 bp    mRNA    linear   EST 26-OCT-2000
DEFINITION  us31g01.x1 Soares_NMEBA_branchial_arch Mus musculus cDNA clone
            IMAGE:3168720 3' similar to TR:Q9VW41 Q9VW41 CG15881 PROTEIN. ;,
            mRNA sequence.
ACCESSION   BF147434
VERSION     BF147434.1  GI:11028829
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml

            MGI:1064180
            High quality sequence stop: 474.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3168720"
                     /tissue_type="branchial arches"
                     /dev_stage="embryo, 10.5 dpc"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="Soares_NMEBA_branchial_arch"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATGCATTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     constructed and normalized by Bento Soares and M.Fatima
                     Bonaldo."
ORIGIN

  Query Match             70.3%;  Score 20.4;  DB 2;  Length 490;
  Best Local Similarity   95.5%;  Pred. No. 5.7e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGG 23
              ||||||||| ||||||||||||
Db        427 ATGGTGATAGGGTAGATACAGG 448


RESULT 14
BX513029/c
LOCUS       BX513029                528 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  BX513029 Soares mouse lymph node NbMLN Mus musculus cDNA clone
            IMAGp952J0565 ; IMAGE:644812, mRNA sequence.
ACCESSION   BX513029
VERSION     BX513029.1  GI:32244756
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
            and Korn,B.
  TITLE     Mouse UnigeneSet - RZPD2
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
```

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp952J0565.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer: T7, Primer sequence: TAATACGACTCACTATAGGG.

FEATURES Location/Qualifiers
source 1. .528
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGp952J0565 ; IMAGE:644812"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse lymph node NbMLN"
/note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGATACTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 70.3%; Score 20.4; DB 5; Length 528;
Best Local Similarity 95.5%; Pred. No. 5.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 ATGGTGATATGGTAGATACAGG 23
              ||||||||| ||||||||||||
Db        127 ATGGTGATAGGGTAGATACAGG 106
```

RESULT 15
CL056918/c
LOCUS CL056918 1020 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-83P3_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-83P3, genomic survey sequence.
ACCESSION CL056918
VERSION CL056918.1 GI:40512831
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1020)
AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
High quality sequence start: 54
High quality sequence stop: 551.

FEATURES Location/Qualifiers
source 1. .1020
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-83P3"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN

Query Match 69.7%; Score 20.2; DB 10; Length 1020;
Best Local Similarity 88.0%; Pred. No. 7.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          3 TGGTGATATGGTAGATACAGGATTT 27
              ||||||| |||||||||  ||||||
Db        844 TGGTGATTTGGTAGATAAGGGATTT 820
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Search completed: March 5, 2006, 23:57:58
Job time : 3173 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 80.5 Seconds
(without alignments)
640.364 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25.8	89.0	38	2	US-08-316-293-53	Sequence 53, Appl
	2	25.8	89.0	386	3	US-09-319-056B-4	Sequence 4, Appli
c	3	25.8	89.0	386	3	US-09-319-056B-6	Sequence 6, Appli
	4	25.8	89.0	1524	2	US-08-409-122-1	Sequence 1, Appli
	5	25.8	89.0	1524	2	US-08-408-669-1	Sequence 1, Appli
	6	25.8	89.0	1524	3	US-08-913-644-1	Sequence 1, Appli
	7	24.2	83.4	410	3	US-09-000-266-7	Sequence 7, Appli
c	8	24.2	83.4	410	3	US-09-000-266-9	Sequence 9, Appli
	9	24.2	83.4	410	3	US-09-628-099-7	Sequence 7, Appli
c	10	24.2	83.4	410	3	US-09-628-099-9	Sequence 9, Appli
	11	24.2	83.4	410	3	US-10-056-360-7	Sequence 7, Appli
c	12	24.2	83.4	410	3	US-10-056-360-9	Sequence 9, Appli
	13	24.2	83.4	410	3	US-10-056-359-7	Sequence 7, Appli
c	14	24.2	83.4	410	3	US-10-056-359-9	Sequence 9, Appli
	15	24.2	83.4	1494	3	US-09-413-611A-5	Sequence 5, Appli
	16	24.2	83.4	1500	3	US-09-413-611A-7	Sequence 7, Appli
	17	24.2	83.4	1517	2	US-08-032-869A-2	Sequence 2, Appli
	18	24.2	83.4	1517	2	US-08-472-673-2	Sequence 2, Appli
	19	24.2	83.4	1517	2	US-08-475-782-2	Sequence 2, Appli
	20	24.2	83.4	1517	2	US-08-472-678-2	Sequence 2, Appli
	21	24.2	83.4	1517	2	US-08-484-503-2	Sequence 2, Appli
	22	24.2	83.4	1518	3	US-08-944-368A-1	Sequence 1, Appli
	23	24.2	83.4	1518	3	US-09-820-764-1	Sequence 1, Appli
	24	24.2	83.4	1518	3	US-09-986-118A-1	Sequence 1, Appli
	25	24.2	83.4	1518	3	US-09-824-017-1	Sequence 1, Appli
	26	22.6	77.9	125	2	US-08-710-082-5	Sequence 5, Appli
c	27	22.6	77.9	125	2	US-08-710-082-20	Sequence 20, Appl
	28	22.6	77.9	125	3	US-08-913-462-5	Sequence 5, Appli
c	29	22.6	77.9	125	3	US-08-913-462-20	Sequence 20, Appl
	30	22.6	77.9	125	3	US-09-624-482-5	Sequence 5, Appli
c	31	22.6	77.9	125	3	US-09-624-482-20	Sequence 20, Appl
	32	22.6	77.9	661	3	US-08-578-634C-3	Sequence 3, Appli
	33	22.6	77.9	661	3	US-09-430-010-3	Sequence 3, Appli
	34	22.6	77.9	662	3	US-08-578-634C-6	Sequence 6, Appli
	35	22.6	77.9	662	3	US-09-430-010-6	Sequence 6, Appli
	36	22.6	77.9	668	3	US-08-578-634C-2	Sequence 2, Appli
	37	22.6	77.9	668	3	US-09-430-010-2	Sequence 2, Appli
	38	22.6	77.9	1059	2	US-08-815-667-11	Sequence 11, Appl
	39	22.6	77.9	1484	3	US-09-210-168-2	Sequence 2, Appli
	40	22.6	77.9	1517	2	US-08-032-869A-1	Sequence 1, Appli
	41	22.6	77.9	1517	2	US-08-472-673-1	Sequence 1, Appli
	42	22.6	77.9	1517	2	US-08-475-782-1	Sequence 1, Appli
	43	22.6	77.9	1517	2	US-08-472-678-1	Sequence 1, Appli
	44	22.6	77.9	1517	2	US-08-484-503-1	Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
US-08-316-293-53
; Sequence 53, Application US/08316293
; Patent No. 5484699
; GENERAL INFORMATION:
;   APPLICANT: ABBOTT LABORATORIES
;   APPLICANT: Stanley R. Bouma
;   APPLICANT: Thomas G. Laffler
;   APPLICANT: Ronald L. Marshall
;   TITLE OF INVENTION: NUCLEOTIDE SEQUENCES USEFUL AS
;   TITLE OF INVENTION: TYPE-SPECIFIC PROBES, PCR PRIMERS AND LCR PROBES
;   TITLE OF INVENTION: FOR THE AMPLIFICATION AND DETECTION OF HUMAN
;   TITLE OF INVENTION: PAPILLOMA VIRUS, AND REALTED KITS AND METHODS.
;   NUMBER OF SEQUENCES: 96
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Abbott Laboratories
;     STREET: One Abbott Park Road
;     CITY: Abbott Park
;     STATE: Illinois
;     COUNTRY: USA
;     ZIP: 60064-3500
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy diskette
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: Wordperfect 5.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/316,293
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/07/965,665
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Thomas D. Brainard
;     REGISTRATION NUMBER: 32,459
;     REFERENCE/DOCKET NUMBER: 4853.US.P1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (708) 937-4884
;     TELEFAX: (708) 937-9556
; INFORMATION FOR SEQ ID NO: 53:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 38
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: Other nucleic acid (synthetic DNA)
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US-08-316-293-53

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Best Local Similarity 93.1%; Pred. No. 0.12;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
US-09-319-056B-4
; Sequence 4, Application US/09319056B
; Patent No. 6413522
; GENERAL INFORMATION:
; APPLICANT: de Villiers-zur Hausen, Ethel-Michele
; APPLICANT: zur Hausen, Harald
; APPLICANT: Lavergne, Donna
; APPLICANT: Benton, Claire
; TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE
; TITLE OF INVENTION: DETECTION THEREOF AS WELL AS FOR TREATING DISEASES CAUSED BY
; TITLE OF INVENTION: THEM
; FILE REFERENCE: 8484-0086-999
; CURRENT APPLICATION NUMBER: US/09/319,056B
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: PCT/DE97/02659
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: DE 196 48 962.8
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Papilloma virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(384)
US-09-319-056B-4

Query Match 89.0%; Score 25.8; DB 3; Length 386;
Best Local Similarity 93.1%; Pred. No. 0.15;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 7 GATGGTGATATGGTAGACATAGGATTTGG 35

RESULT 3
US-09-319-056B-6/c
; Sequence 6, Application US/09319056B
; Patent No. 6413522
; GENERAL INFORMATION:
; APPLICANT: de Villiers-zur Hausen, Ethel-Michele
; APPLICANT: zur Hausen, Harald
; APPLICANT: Lavergne, Donna
; APPLICANT: Benton, Claire
; TITLE OF INVENTION: PAPILLOMA VIRUSES, PRODUCTS FOR THE
; TITLE OF INVENTION: DETECTION THEREOF AS WELL AS FOR TREATING DISEASES CAUSED BY
; TITLE OF INVENTION: THEM
; FILE REFERENCE: 8484-0086-999
; CURRENT APPLICATION NUMBER: US/09/319,056B
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: PCT/DE97/02659
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: DE 196 48 962.8
; PRIOR FILING DATE: 1996-11-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 386
; TYPE: DNA
; ORGANISM: Papilloma virus
US-09-319-056B-6

Query Match 89.0%; Score 25.8; DB 3; Length 386;
Best Local Similarity 93.1%; Pred. No. 0.15;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db 380 GATGGTGATATGGTAGACATAGGATTTGG 352

RESULT 4
US-08-409-122-1
; Sequence 1, Application US/08409122
; Patent No. 5820870
; GENERAL INFORMATION:
; APPLICANT: JOYCE, JAMES G.
; APPLICANT: GEORGE, HUGH A.
; APPLICANT: HOFMANN, KATHRYN J.
; APPLICANT: JANSEN, KATHRIN U.
; APPLICANT: NEEPER, MICHAEL P.
; TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18 VACCINE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/409,122
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/408,669
; FILING DATE: 22-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19425
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-6734
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-409-122-1

Query Match 89.0%; Score 25.8; DB 2; Length 1524;
Best Local Similarity 93.1%; Pred. No. 0.18;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 589 GATGGTGATATGGTAGATACTGGATATGG 617

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RESULT 5
US-08-408-669-1
; Sequence 1, Application US/08408669
; Patent No. 5840306
;  GENERAL INFORMATION:
;    APPLICANT:  HOFMANN, KATHRYN J.
;    APPLICANT:  JANSEN, KATHRIN U.
;    APPLICANT:  NEEPER, MICHAEL P.
;    TITLE OF INVENTION:  DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE 18
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHRISTINE E. CARTY - MERCK & CO., INC.
;      STREET:  126 EAST LINCOLN AVENUE - P.O. BOX 2000
;      CITY:  RAHWAY
;      STATE:  NJ
;      COUNTRY:  US
;      ZIP:  07065-0907
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/408,669
;      FILING DATE:  22-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CARTY, CHRISTINE E
;      REGISTRATION NUMBER:  36,099
;      REFERENCE/DOCKET NUMBER:  19424
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  908-594-6734
;      TELEFAX:  908-594-4720
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1524 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-408-669-1

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  Best Local Similarity   93.1%;  Pred. No. 0.18;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||| |||| |||
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RESULT 6
US-08-913-644-1
; Sequence 1, Application US/08913644
; Patent No. 6908615
; GENERAL INFORMATION:
;  APPLICANT: Hofmann, Kathryn J.
;  APPLICANT:  Jansen, Kathrin U.
;  APPLICANT:  Neeper, Michael P.
;  TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE
;  TITLE OF INVENTION:  18
;  FILE REFERENCE: 19424PC
;  CURRENT APPLICATION NUMBER: US/08/913,644
;  CURRENT FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/US96/03649
;  PRIOR FILING DATE: 1996-03-18
;  PRIOR APPLICATION NUMBER: 08/408,669
;  PRIOR FILING DATE: 1995-03-22
;  PRIOR APPLICATION NUMBER: 08/409,122
;  PRIOR FILING DATE: 1995-03-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HPV18 L1 Consensus Sequence
US-08-913-644-1

  Query Match             89.0%;  Score 25.8;  DB 3;  Length 1524;
  Best Local Similarity   93.1%;  Pred. No. 0.18;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db        589 GATGGTGATATGGTAGATACTGGATATGG 617


RESULT 7
US-09-000-266-7
; Sequence 7, Application US/09000266A
; Patent No. 6322795
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT: Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/09/000,266A
;  CURRENT FILING DATE: 1998-10-19
;  EARLIER APPLICATION NUMBER: PCT/DE96/01369
;  EARLIER FILING DATE: 1996-07-19
;  EARLIER APPLICATION NUMBER: DE P 195 26 386.3
;  EARLIER FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-09-000-266-7

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  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 8
US-09-000-266-9/c
; Sequence 9, Application US/09000266A
; Patent No. 6322795
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT: De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT: Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION: THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
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;  CURRENT APPLICATION NUMBER: US/09/000,266A
;  CURRENT FILING DATE: 1998-10-19
;  EARLIER APPLICATION NUMBER: PCT/DE96/01369
;  EARLIER FILING DATE: 1996-07-19
;  EARLIER APPLICATION NUMBER: DE P 195 26 386.3
;  EARLIER FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-09-000-266-9

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||  ||||  |||||||||
Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 9
US-09-628-099-7
; Sequence 7, Application US/09628099
; Patent No. 6368832
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/09/628,099
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-09-628-099-7

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 10
US-09-628-099-9/c
; Sequence 9, Application US/09628099
; Patent No. 6368832
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/09/628,099
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-09-628-099-9

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 11
US-10-056-360-7
; Sequence 7, Application US/10056360
; Patent No. 6555345
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,360
;  CURRENT FILING DATE:  2000-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-10-056-360-7

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||  ||||  |||||||||
Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 12
US-10-056-360-9/c
; Sequence 9, Application US/10056360
; Patent No. 6555345
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,360
;  CURRENT FILING DATE:  2000-01-23
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;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-10-056-360-9

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||| |||| |||||||||
Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 13
US-10-056-359-7
; Sequence 7, Application US/10056359
; Patent No. 6562597
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,359
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2001-05-08
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-10-056-359-7

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||| |||| |||||||||
Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 14
US-10-056-359-9/c
; Sequence 9, Application US/10056359
; Patent No. 6562597
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,359
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2001-05-08
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-10-056-359-9

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 0.71;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||| |||| |||||||||
Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 15
US-09-413-611A-5
; Sequence 5, Application US/09413611A
; Patent No. 6380364
; GENERAL INFORMATION:
;  APPLICANT:  Mueller, Martin
;  APPLICANT:  Kast, Wijbe
;  APPLICANT:  Nieland, John
;  APPLICANT:  Velders, Markwin
;  TITLE OF INVENTION:  Chimeric Biotin-Binding Papillomavirus Protein
;  FILE REFERENCE:  202325
;  CURRENT APPLICATION NUMBER: US/09/413,611A
;  CURRENT FILING DATE:  1999-10-06
;  PRIOR APPLICATION NUMBER:  US 60/109,510
;  PRIOR FILING DATE:  1998-11-23
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1494
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:biotin-binding
;   OTHER INFORMATION: papillomavirus protein 168
;   NAME/KEY: CDS
;   LOCATION: (1)..(1491)
US-09-413-611A-5

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1494;
  Best Local Similarity   89.7%;  Pred. No. 0.81;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||| ||||| || ||||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


Search completed: March  5, 2006, 19:13:35
Job time : 81.5 secs
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:00:24 ; Search time 361 Seconds
(without alignments)
664.299 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	29	8	US-10-720-424B-1	Sequence 1, Appli
	2	25.8	89.0	1421	7	US-10-433-091-1	Sequence 1, Appli
	3	24.2	83.4	410	5	US-10-056-359-7	Sequence 7, Appli
c	4	24.2	83.4	410	5	US-10-056-359-9	Sequence 9, Appli
	5	24.2	83.4	410	5	US-10-056-360-7	Sequence 7, Appli
c	6	24.2	83.4	410	5	US-10-056-360-9	Sequence 9, Appli
	7	24.2	83.4	1452	9	US-10-487-719-2	Sequence 2, Appli
	8	24.2	83.4	1452	9	US-10-487-719-4	Sequence 4, Appli
	9	24.2	83.4	1517	3	US-09-832-065-2	Sequence 2, Appli
	10	24.2	83.4	1517	6	US-10-371-846-2	Sequence 2, Appli
	11	24.2	83.4	1518	3	US-09-820-765-1	Sequence 1, Appli
	12	24.2	83.4	1518	3	US-09-162-904A-1	Sequence 1, Appli
	13	24.2	83.4	1518	3	US-09-162-904A-2	Sequence 2, Appli
	14	24.2	83.4	1518	3	US-09-824-017-1	Sequence 1, Appli
	15	24.2	83.4	1518	3	US-09-986-118A-1	Sequence 1, Appli
	16	24.2	83.4	1518	6	US-10-367-095-11	Sequence 11, Appl
	17	24.2	83.4	1518	7	US-10-368-046-11	Sequence 11, Appl
	18	24.2	83.4	1518	7	US-10-654-129-1	Sequence 1, Appli
	19	24.2	83.4	1518	7	US-10-367-367-11	Sequence 11, Appl
	20	24.2	83.4	1518	8	US-10-042-526A-1	Sequence 1, Appli
	21	24.2	83.4	1518	9	US-10-487-719-1	Sequence 1, Appli
	22	24.2	83.4	1518	9	US-10-487-719-3	Sequence 3, Appli
	23	24.2	83.4	1518	9	US-10-918-337-11	Sequence 11, Appl
	24	24.2	83.4	1890	3	US-09-864-408A-8573	Sequence 8573, Ap
	25	22.6	77.9	1404	8	US-10-475-203A-7	Sequence 7, Appli
	26	22.6	77.9	1484	3	US-09-970-477-2	Sequence 2, Appli
	27	22.6	77.9	1503	8	US-10-475-203A-3	Sequence 3, Appli
	28	22.6	77.9	1517	3	US-09-832-065-1	Sequence 1, Appli
	29	22.6	77.9	1517	6	US-10-371-846-1	Sequence 1, Appli
	30	22.6	77.9	1518	6	US-10-367-095-12	Sequence 12, Appl
	31	22.6	77.9	1518	7	US-10-368-046-12	Sequence 12, Appl
	32	22.6	77.9	1518	7	US-10-367-367-12	Sequence 12, Appl
	33	22.6	77.9	1518	9	US-10-918-337-12	Sequence 12, Appl
	34	22.6	77.9	1596	9	US-10-367-057-115	Sequence 115, App
	35	22.6	77.9	7904	9	US-10-494-800-2	Sequence 2, Appli
	36	21.2	73.1	1849	5	US-10-112-178-1	Sequence 1, Appli
	37	21	72.4	398	5	US-10-056-359-28	Sequence 28, Appl
c	38	21	72.4	398	5	US-10-056-359-30	Sequence 30, Appl
	39	21	72.4	398	5	US-10-056-360-28	Sequence 28, Appl
c	40	21	72.4	398	5	US-10-056-360-30	Sequence 30, Appl
	41	21	72.4	416	5	US-10-056-359-22	Sequence 22, Appl
c	42	21	72.4	416	5	US-10-056-359-24	Sequence 24, Appl
	43	21	72.4	416	5	US-10-056-360-22	Sequence 22, Appl
c	44	21	72.4	416	5	US-10-056-360-24	Sequence 24, Appl
	45	21	72.4	425	5	US-10-056-359-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-720-424B-1
; Sequence 1, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-1

Query Match 100.0%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||||||||||||||||||
Db 1 GATGGTGATATGGTAGATACAGGATTTGG 29

RESULT 2
US-10-433-091-1
; Sequence 1, Application US/10433091
; Publication No. US20040101533A1
; GENERAL INFORMATION:
; APPLICANT: MULLER, RAINER
; APPLICANT: NIELAND, JOHN
; APPLICANT: GABELSBERGER, JOSEF

```
;  APPLICANT:  HERBST, RUTH
;  TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
;  TITLE OF INVENTION:  HUMAN PAPILLOMAVIRUS TYPE 18
;  FILE REFERENCE: 037067/0115
;  CURRENT APPLICATION NUMBER: US/10/433,091
;  CURRENT FILING DATE:  2003-11-25
;  PRIOR APPLICATION NUMBER: PCT/EP01/14038
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: DE 100 59 630.4
;  PRIOR FILING DATE: 2000-12-01
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1421
;   TYPE: DNA
;   ORGANISM: Human papillomavirus type 18
US-10-433-091-1

  Query Match             89.0%;  Score 25.8;  DB 7;  Length 1421;
  Best Local Similarity   93.1%;  Pred. No. 1.2;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||||||||| |||| |||
Db        589 GATGGTGATATGGTAGATACTGGATATGG 617


RESULT 3
US-10-056-359-7
; Sequence 7, Application US/10056359
; Publication No. US20020110865A1
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,359
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2001-05-08
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-10-056-359-7

  Query Match             83.4%;  Score 24.2;  DB 5;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 4.4;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||  |||| |||||||||
Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 4
US-10-056-359-9/c
; Sequence 9, Application US/10056359
; Publication No. US20020110865A1
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,359
;  CURRENT FILING DATE:  2002-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2001-05-08
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-10-056-359-9

  Query Match             83.4%;  Score 24.2;  DB 5;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 4.4;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||  |||| |||||||||
Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 5
US-10-056-360-7
; Sequence 7, Application US/10056360
; Publication No. US20020110866A1
; GENERAL INFORMATION:
;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,360
;  CURRENT FILING DATE:  2000-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(408)
US-10-056-360-7

  Query Match             83.4%;  Score 24.2;  DB 5;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 4.4;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||  |||| |||||||||
Db         13 GATGGTGATATGGGTGATATAGGATTTGG 41


RESULT 6
US-10-056-360-9/c
; Sequence 9, Application US/10056360
; Publication No. US20020110866A1
; GENERAL INFORMATION:
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;  APPLICANT: Shamanin, Vladimir
;  APPLICANT:  De Villiers-Zur Hausen, Ethel-Michele
;  APPLICANT:  Zur Hausen, Harald
;  TITLE OF INVENTION: PAPILLOMA VIRUSES, AGENTS FOR DETECTING
;  TITLE OF INVENTION:  THEM AND FOR TREATING DISEASES CAUSED BY SUCH VIRUSES
;  FILE REFERENCE: 8484-0037-999
;  CURRENT APPLICATION NUMBER: US/10/056,360
;  CURRENT FILING DATE:  2000-01-23
;  PRIOR APPLICATION NUMBER: US/09/628,099
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/000,266
;  PRIOR FILING DATE: 1998-10-19
;  PRIOR APPLICATION NUMBER: DE P 195 26 386.3
;  PRIOR FILING DATE: 1995-07-19
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 410
;   TYPE: DNA
;   ORGANISM: Papilloma virus
US-10-056-360-9

  Query Match             83.4%;  Score 24.2;  DB 5;  Length 410;
  Best Local Similarity   89.7%;  Pred. No. 4.4;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||  |||| |||||||||
Db        398 GATGGTGATATGGGTGATATAGGATTTGG 370


RESULT 7
US-10-487-719-2
; Sequence 2, Application US/10487719
; Publication No. US20050090435A1
; GENERAL INFORMATION:
;  APPLICANT: Varsani, Arvind
;  APPLICANT:  Tybicki, Edward
;  APPLICANT:  Williamson, Anna-Lise
;  TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
;  TITLE OF INVENTION:  Isolating Said Pharmaceutical Compositions, and Use of Said
;  TITLE OF INVENTION:  Pharmaceutical Compositions for Prophylactic Treatment of
;  TITLE OF INVENTION:  Lesions and Carcinomas
;  FILE REFERENCE: 025455-116
;  CURRENT APPLICATION NUMBER: US/10/487,719
;  CURRENT FILING DATE:  2004-02-27
;  PRIOR APPLICATION NUMBER: PCT/IB02/03531
;  PRIOR FILING DATE: 2002-08-30
;  PRIOR APPLICATION NUMBER: ZA 2001/7228
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fragment of L1 gene
US-10-487-719-2

  Query Match             83.4%;  Score 24.2;  DB 9;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 8
US-10-487-719-4
; Sequence 4, Application US/10487719
; Publication No. US20050090435A1
; GENERAL INFORMATION:
;  APPLICANT: Varsani, Arvind
;  APPLICANT:  Tybicki, Edward
;  APPLICANT:  Williamson, Anna-Lise
;  TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
;  TITLE OF INVENTION:  Isolating Said Pharmaceutical Compositions, and Use of Said
;  TITLE OF INVENTION:  Pharmaceutical Compositions for Prophylactic Treatment of
;  TITLE OF INVENTION:  Lesions and Carcinomas
;  FILE REFERENCE: 025455-116
;  CURRENT APPLICATION NUMBER: US/10/487,719
;  CURRENT FILING DATE:  2004-02-27
;  PRIOR APPLICATION NUMBER: PCT/IB02/03531
;  PRIOR FILING DATE: 2002-08-30
;  PRIOR APPLICATION NUMBER: ZA 2001/7228
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fragment of L1 gene
US-10-487-719-4

  Query Match             83.4%;  Score 24.2;  DB 9;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 9
US-09-832-065-2
; Sequence 2, Application US/09832065
; Publication No. US20030050439A1
;  GENERAL INFORMATION:
;       APPLICANT: Lowy, Douglas R.
;                  Schiller, John T.
;                  Kirnbauer, Reinhard
;       TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                           PAPILLOMAVIRUS CAPSID PROTEINS
;       NUMBER OF SEQUENCES: 6
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;            STREET: 620 Newport Center Drive, Sixteenth Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/832,065
;            FILING DATE: 09-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/316,487
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kirkpatrick Ph.D., Anita M.
;            REGISTRATION NUMBER: 32,617
;            REFERENCE/DOCKET NUMBER: NIH032.001CP1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 619-235-8550
;            TELEFAX: 619-235-0176
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
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;             LENGTH: 1517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;          MOLECULE TYPE: DNA (genomic)
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FEATURE:
;               NAME/KEY:  CDS
;               LOCATION:  1..1517
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-832-065-2

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 10
US-10-371-846-2
; Sequence 2, Application US/10371846
; Publication No. US20030219873A1
;   GENERAL INFORMATION:
;          APPLICANT: Lowy, Douglas R.
;                     Schiller, John T.
;                     Kirnbauer, Reinhard
;          TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                              PAPILLOMAVIRUS CAPSID PROTEINS
;          NUMBER OF SEQUENCES: 6
;          CORRESPONDENCE ADDRESS:
;               ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;               STREET: 620 Newport Center Drive, Sixteenth Floor
;               CITY: Newport Beach
;               STATE: CA
;               COUNTRY: USA
;               ZIP: 92660
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.25
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/10/371,846
;               FILING DATE: 21-Feb-2003
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: US/08/032,869
;               FILING DATE: 16-MAR-1993
;               APPLICATION NUMBER: US 07/941,371
;               FILING DATE: 03-SEP-1992
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Kirkpatrick Ph.D., Anita M.
;               REGISTRATION NUMBER: 32,617
;               REFERENCE/DOCKET NUMBER: NIH032.001CP1
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: 619-235-8550
;               TELEFAX: 619-235-0176
;     INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 1517 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          MOLECULE TYPE: DNA (genomic)
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FEATURE:
;               NAME/KEY:  CDS
;               LOCATION:  1..1517
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-371-846-2

  Query Match             83.4%;  Score 24.2;  DB 6;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 11
US-09-820-765-1
; Sequence 1, Application US/09820765
; Publication No. US20020039584A1
;   GENERAL INFORMATION:
;          APPLICANT: BURGER, Alexander
;                     HALLEK, Michael
;          TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                              FORMULATIONS AND METHODS OF USE
;          NUMBER OF SEQUENCES: 28
;          CORRESPONDENCE ADDRESS:
;               ADDRESSEE: FOLEY & LARDNER
;               STREET: 3000 K Street, N.W.
;               CITY: Washington
;               STATE: D.C.
;               COUNTRY: U.S.A.
;               ZIP: 20007-5109
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/09/820,765
;               FILING DATE: 30-Mar-2001
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: US 09/026,896
;               FILING DATE: 20-FEB-1998
;          ATTORNEY/AGENT INFORMATION:
;               NAME: Sandercock, Colin G.
;               REGISTRATION NUMBER: 31,298
;               REFERENCE/DOCKET NUMBER: 37067/102
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (202) 672-5300
;               TELEFAX: (202) 672-5399
;     INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 1518 base pairs
;               TYPE: nucleic acid
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;          MOLECULE TYPE: DNA (genomic)
;          FEATURE:
;               NAME/KEY:  CDS
;               LOCATION:  1..1515
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-765-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 12
US-09-162-904A-1
; Sequence 1, Application US/09162904A
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; Patent No. US20020168372A1
; GENERAL INFORMATION:
;  APPLICANT: Durst, Matthias
;  APPLICANT:  Gissmann, Lutz
;  TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
;  TITLE OF INVENTION:  OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
;  FILE REFERENCE: 8484-068-999
;  CURRENT APPLICATION NUMBER: US/09/162,904A
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 08/884,168
;  PRIOR FILING DATE: 1997-06-27
;  PRIOR APPLICATION NUMBER: 08/641,570
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/902,528
;  PRIOR FILING DATE: 1993-07-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gen
;   OTHER INFORMATION: HPV16 DNA clone P114/16/2
US-09-162-904A-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 13
US-09-162-904A-2
; Sequence 2, Application US/09162904A
; Patent No. US20020168372A1
; GENERAL INFORMATION:
;  APPLICANT: Durst, Matthias
;  APPLICANT:  Gissmann, Lutz
;  TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
;  TITLE OF INVENTION:  OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
;  FILE REFERENCE: 8484-068-999
;  CURRENT APPLICATION NUMBER: US/09/162,904A
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 08/884,168
;  PRIOR FILING DATE: 1997-06-27
;  PRIOR APPLICATION NUMBER: 08/641,570
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/902,528
;  PRIOR FILING DATE: 1993-07-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gen
;   OTHER INFORMATION: HPV16 DNA clone P114/16/11
US-09-162-904A-2

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 14
US-09-824-017-1
; Sequence 1, Application US/09824017
; Publication No. US20020197668A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/824,017
;             FILING DATE: 03-Apr-2001
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/026,896
;             FILING DATE: 1998-02-20
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-824-017-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 15
US-09-986-118A-1
; Sequence 1, Application US/09986118A
; Publication No. US20030021806A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
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;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/986,118A
;             FILING DATE: 07-No. US20030021806A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/026,896
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-986-118A-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 5.5;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


Search completed: March  5, 2006, 22:49:27
Job time : 362 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:06:14 ; Search time 457 Seconds
(without alignments)
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Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24.2	83.4	1518	7	US-10-514-878A-2	Sequence 2, Appli
	2	24.2	83.4	1518	7	US-10-514-878A-4	Sequence 4, Appli
	3	24.2	83.4	1518	7	US-10-514-878A-6	Sequence 6, Appli
	4	24.2	83.4	1518	7	US-10-514-878A-8	Sequence 8, Appli
	5	24.2	83.4	1518	7	US-10-514-878A-10	Sequence 10, Appl
	6	24.2	83.4	1518	7	US-10-514-878A-12	Sequence 12, Appl
	7	24.2	83.4	1518	12	US-11-179-478-1	Sequence 1, Appli
	8	19.6	67.6	623	6	US-09-925-065A-809541	Sequence 809541,
	9	19.2	66.2	610	6	US-09-925-065A-883719	Sequence 883719,
c	10	19	65.5	200	12	US-11-098-686-6941	Sequence 6941, Ap
c	11	19	65.5	596	6	US-09-925-065A-717454	Sequence 717454,
	12	19	65.5	617	6	US-09-925-065A-575086	Sequence 575086,
	13	19	65.5	622	6	US-09-925-065A-762355	Sequence 762355,
	14	19	65.5	1926	12	US-11-098-686-9784	Sequence 9784, Ap
	15	19	65.5	27733	8	US-10-829-826B-18	Sequence 18, Appl
c	16	19	65.5	1457619	12	US-11-098-686-8739	Sequence 8739, Ap
c	17	18.6	64.1	502	6	US-09-925-065A-551876	Sequence 551876,
c	18	18.6	64.1	556	6	US-09-925-065A-484856	Sequence 484856,
	19	18.6	64.1	159138	8	US-10-995-561-13230	Sequence 13230, A
c	20	18.6	64.1	159781	12	US-11-121-086-92	Sequence 92, Appl
	21	18.4	63.4	550	6	US-09-925-065A-821943	Sequence 821943,
	22	18.4	63.4	585	6	US-09-925-065A-561682	Sequence 561682,
	23	18.4	63.4	585	6	US-09-925-065A-561683	Sequence 561683,
c	24	18.4	63.4	654	6	US-09-925-065A-111263	Sequence 111263,
	25	18.2	62.8	599	6	US-09-925-065A-899601	Sequence 899601,
	26	18.2	62.8	599	6	US-09-925-065A-899602	Sequence 899602,
	27	18.2	62.8	645	6	US-09-925-065A-233861	Sequence 233861,
	28	18.2	62.8	645	6	US-09-925-065A-233862	Sequence 233862,
	29	18.2	62.8	1314	6	US-09-925-065A-3498	Sequence 3498, Ap
	30	18	62.1	560	6	US-09-925-065A-652774	Sequence 652774,
c	31	18	62.1	579	12	US-11-128-061-1855	Sequence 1855, Ap
c	32	18	62.1	579	12	US-11-128-061-5497	Sequence 5497, Ap
c	33	18	62.1	579	12	US-11-128-049-1855	Sequence 1855, Ap
c	34	18	62.1	579	12	US-11-128-049-5497	Sequence 5497, Ap
	35	18	62.1	661	6	US-09-925-065A-875490	Sequence 875490,
c	36	18	62.1	773	6	US-09-925-065A-34733	Sequence 34733, A
	37	18	62.1	1233	6	US-09-925-065A-713292	Sequence 713292,
	38	18	62.1	1446	8	US-10-750-185-25879	Sequence 25879, A
	39	18	62.1	1446	8	US-10-750-623-25879	Sequence 25879, A
	40	18	62.1	1538	8	US-10-750-185-38674	Sequence 38674, A
	41	18	62.1	1538	8	US-10-750-623-38674	Sequence 38674, A
	42	18	62.1	2392	8	US-10-750-185-26754	Sequence 26754, A
	43	18	62.1	2392	8	US-10-750-623-26754	Sequence 26754, A
c	44	18	62.1	3771	6	US-09-925-065A-727856	Sequence 727856,
	45	18	62.1	57889	7	US-10-330-773-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-514-878A-2
; Sequence 2, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Me
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-2

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617
```

RESULT 2
US-10-514-878A-4
; Sequence 4, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Me
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1518

; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-4

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||| ||||| || |||||
Db 589 GATGGTGATATGGTTGATACTGGCTTTGG 617

RESULT 3
US-10-514-878A-6
; Sequence 6, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-6

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||| ||||| || |||||
Db 589 GATGGTGATATGGTTGATACTGGCTTTGG 617

RESULT 4
US-10-514-878A-8
; Sequence 8, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-8

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||| ||||| || |||||
Db 589 GATGGTGATATGGTTGATACTGGCTTTGG 617

RESULT 5
US-10-514-878A-10
; Sequence 10, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Me
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-10

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||| ||||| || |||||
Db 589 GATGGTGATATGGTTGATACTGGCTTTGG 617

RESULT 6
US-10-514-878A-12
; Sequence 12, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Me
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-12

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.72;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GATGGTGATATGGTAGATACAGGATTTGG 29
||||||||||||||| ||||| || |||||
Db 589 GATGGTGATATGGTTGATACTGGCTTTGG 617

RESULT 7
US-11-179-478-1
; Sequence 1, Application US/11179478
; Publication No. US20050249745A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/179,478
;      FILING DATE:  13-JULY-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/654,129
;      FILING DATE:  04-Sep-2003
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sandercock, Colin G.
;      REGISTRATION NUMBER:  31,298
;      REFERENCE/DOCKET NUMBER:  37067/102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 672-5300
;      TELEFAX:  (202) 672-5399
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1518 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1515
US-11-179-478-1

  Query Match             83.4%;  Score 24.2;  DB 12;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.72;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||||||||||||||| ||||| || |||||
Db        589 GATGGTGATATGGTTGATACTGGCTTTGG 617


RESULT 8
US-09-925-065A-809541
; Sequence 809541, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 809541
;   LENGTH: 623
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-809541

  Query Match             67.6%;  Score 19.6;  DB 6;  Length 623;
  Best Local Similarity   84.6%;  Pred. No. 59;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATT 26
              ||||||| | || |||||| ||||||
Db        564 GATGGTGCTGTGCTAGATATAGGATT 589


RESULT 9
US-09-925-065A-883719
; Sequence 883719, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 883719
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-883719

  Query Match             66.2%;  Score 19.2;  DB 6;  Length 610;
  Best Local Similarity   87.5%;  Pred. No. 88;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 TGGTGATATGGTAGATACAGGATT 26
              |||||||||||||| ||| | ||
Db        409 TGGTGATATGGTAGAAACATGGTT 432


RESULT 10
US-11-098-686-6941/c
; Sequence 6941, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6941
;   LENGTH: 200
;   TYPE: DNA
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-6941

  Query Match             65.5%;  Score 19;  DB 12;  Length 200;
  Best Local Similarity   81.5%;  Pred. No. 82;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGGATTTG 28
              ||||| |||| ||||| |||| || ||
Db        199 ATGGTAATATAGTAGAAACAGCATATG 173


RESULT 11
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```
US-09-925-065A-717454/c
; Sequence 717454, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 717454
;   LENGTH: 596
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-717454

  Query Match             65.5%;  Score 19;  DB 6;  Length 596;
  Best Local Similarity   75.9%;  Pred. No. 1.1e+02;
  Matches   22;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              ||| |||||||:| || ||||| | | ||
Db        119 GATAGTGATATRGCAGGTACAGTAATAGG 91


RESULT 12
US-09-925-065A-575086
; Sequence 575086, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 575086
;   LENGTH: 617
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-575086

  Query Match             65.5%;  Score 19;  DB 6;  Length 617;
  Best Local Similarity   81.5%;  Pred. No. 1.1e+02;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTT 27
              | |||||||| || |||| ||||| ||
Db        419 GCTGGTGATAGGGCAGATTCAGGAATT 445


RESULT 13
US-09-925-065A-762355
; Sequence 762355, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 762355
;   LENGTH: 622
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-762355

  Query Match             65.5%;  Score 19;  DB 6;  Length 622;
  Best Local Similarity   81.5%;  Pred. No. 1.1e+02;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTT 27
              | |||||||| || |||| ||||| ||
Db        563 GCTGGTGATAGGGCAGATTCAGGAATT 589


RESULT 14
US-11-098-686-9784
; Sequence 9784, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9784
;   LENGTH: 1926
;   TYPE: DNA
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-9784

  Query Match             65.5%;  Score 19;  DB 12;  Length 1926;
  Best Local Similarity   81.5%;  Pred. No. 1.4e+02;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ATGGTGATATGGTAGATACAGGATTTG 28
              ||||| |||| ||||| |||| || ||
Db        683 ATGGTAATATAGTAGAAACAGCATATG 709


RESULT 15
```

```
US-10-829-826B-18
; Sequence 18, Application US/10829826B
; Publication No. US20050266397A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, David J.
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Blyn, Lawrence B.
;  APPLICANT:  Hall, Thomas A.
;  APPLICANT:  Massire, Christian
;  TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF CORONAVIRUSES
;  FILE REFERENCE: IBIS0075-100 (DIBIS-0058US)
;  CURRENT APPLICATION NUMBER: US/10/829,826B
;  CURRENT FILING DATE:  2004-04-22
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 27733
;   TYPE: DNA
;   ORGANISM: Coronavirus
US-10-829-826B-18

  Query Match             65.5%;  Score 19;  DB 8;  Length 27733;
  Best Local Similarity   81.5%;  Pred. No. 2.8e+02;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 TGGTGATATGGTAGATACAGGATTTGG 29
              |||| |||  ||||||  |||||||||
Db      26684 TGGTTATAGAGTAGATCAAGGATTTGG 26710


Search completed: March  5, 2006, 22:37:00
Job time : 459 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:50:08 ; Search time 380.5 Seconds
(without alignments)
507.953 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	100.0	29	12	ADQ27978	Adq27978 Human pap
c 2	24.2	83.4	1452	10	ACC47503	Acc47503 HPV 16 L1
c 3	24.2	83.4	1452	10	ACC47505	Acc47505 HPV 16 L1
c 4	24.2	83.4	1484	2	AAX89755	Aax89755 Probe seq
c 5	24.2	83.4	1494	3	AAD01237	Aad01237 Chimeric
c 6	24.2	83.4	1500	3	AAD01238	Aad01238 Chimeric
c 7	24.2	83.4	1517	2	AAQ47167	Aaq47167 HPV1 L1 O
c 8	24.2	83.4	1517	2	AAQ47166	Aaq47166 BPV1 L1 O
c 9	24.2	83.4	1517	2	AAV09856	Aav09856 HPV16 rec
c 10	24.2	83.4	1517	2	AAV09855	Aav09855 HPV16 L1
c 11	24.2	83.4	1517	2	AAV25818	Aav25818 Human pap
c 12	24.2	83.4	1517	2	AAV25817	Aav25817 Human pap
c 13	24.2	83.4	1517	2	AAV12161	Aav12161 Human pap
c 14	24.2	83.4	1517	2	AAV12162	Aav12162 Human pap
c 15	24.2	83.4	1517	2	AAV23923	Aav23923 HPV16 L1
c 16	24.2	83.4	1517	2	AAV24099	Aav24099 HPV16 L1
c 17	24.2	83.4	1517	2	AAX15111	Aax15111 Human pap
c 18	24.2	83.4	1517	2	AAX15112	Aax15112 Human pap
c 19	24.2	83.4	1517	3	AAZ40564	Aaz40564 HPV16 L1
c 20	24.2	83.4	1517	3	AAZ40563	Aaz40563 HPV16 L1
c 21	24.2	83.4	1517	10	ADC26168	Adc26168 HPV16 L1
c 22	24.2	83.4	1517	10	ADC26169	Adc26169 HPV16 L1
c 23	24.2	83.4	1517	12	ADG62855	Adg62855 Human pap
c 24	24.2	83.4	1517	12	ADG62854	Adg62854 DNA encod
c 25	24.2	83.4	1518	2	AAX37566	Aax37566 Human pap
c 26	24.2	83.4	1518	3	AAZ48174	Aaz48174 Human pap
c 27	24.2	83.4	1518	9	ABX11395	Abx11395 Human pap
c 28	24.2	83.4	1518	9	ABX11396	Abx11396 Human pap
c 29	24.2	83.4	1518	9	ADA27368	Ada27368 HPV-16 L1
c 30	24.2	83.4	1518	9	ADA27369	Ada27369 HPV-16 L1
c 31	24.2	83.4	1518	9	ADA92547	Ada92547 HPV-16 L1
c 32	24.2	83.4	1518	9	ADA92546	Ada92546 HPV-16 L1
c 33	24.2	83.4	1518	9	ADA14296	Ada14296 HPV-16 L1
c 34	24.2	83.4	1518	9	ADA14295	Ada14295 HPV-16 L1
c 35	24.2	83.4	1518	9	AAD58576	Aad58576 HPV-16 L1
c 36	24.2	83.4	1518	9	AAD58577	Aad58577 HPV-16 L1
c 37	24.2	83.4	1518	10	ACC47502	Acc47502 HPV 16 L1
c 38	24.2	83.4	1518	10	ACC47504	Acc47504 HPV 16 L1
c 39	24.2	83.4	1518	12	ADF83436	Adf83436 Human pap
c 40	24.2	83.4	1518	12	ADF83440	Adf83440 Human pap
c 41	24.2	83.4	1518	12	ADF83438	Adf83438 Human pap
c 42	24.2	83.4	1518	12	ADF83434	Adf83434 Human pap
c 43	24.2	83.4	1518	12	ADF83444	Adf83444 Human pap
c 44	24.2	83.4	1518	12	ADF83442	Adf83442 Human pap
c 45	24.2	83.4	1518	12	ADN49002	Adn49002 Human pap

ALIGNMENTS

RESULT 1
ADQ27978
ID ADQ27978 standard; DNA; 29 BP.
XX
AC ADQ27978;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human papillomavirus genotype detection PCR primer #8.
XX
KW ss; primer; detection; diagnosis; amplification;
KW Human Papillomavirus genotype; cervical-neoplasia;
KW oncogenic high-risk group.
XX
OS Human papillomavirus.
XX
PN WO2004050917-A1.
XX
PD 17-JUN-2004.
XX
PF 28-NOV-2003; 2003WO-KR002608.
XX
PR 29-NOV-2002; 2002KR-00075370.
PR 31-JUL-2003; 2003KR-00053147.
XX
PA (ALBI-) ALBIOMED CO LTD.
XX
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;
XX
DR WPI; 2004-450746/42.
XX
PT New general primer or primer pair, useful for amplifying and detecting,
PT or for use in a nucleic acid amplification process for amplifying Human
PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT genotypes.
XX
PS Claim 2; SEQ ID NO 8; 71pp; English.
XX
CC The invention relates to a general primer or primer pair for amplifying
CC and detecting or for use in a nucleic acid amplification process for
CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC useful for amplifying cervical-neoplasia related HPV genotypes including

```
CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 29 BP; 8 A; 7 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 12;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00036;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              |||||||||||||||||||||||||||||
Db          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29


RESULT 2
ACC47503/c
ID   ACC47503 standard; DNA; 1452 BP.
XX
AC   ACC47503;
XX
DT   27-JUN-2003  (first entry)
XX
DE   HPV 16 L1 capsid protein gene SA-L1-NLS.
XX
KW   L1 capsid protein; HPV 16; virucide; immunostimulant; gene therapy;
KW   vaccine; cervical lesion; carcinoma; gene; ds.
XX
OS   Human papillomavirus.
XX
PN   WO2003018623-A2.
XX
PD   06-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-IB003531.
XX
PR   31-AUG-2001; 2001ZA-00007228.
XX
PA   (UYCA-) UNIV CAPE TOWN.
XX
PI   Varsani AD,  Rybicki EP,  Williamson A;
XX
DR   WPI; 2003-290048/28.
XX
PT   New nucleotide sequence encoding papillomavirus protein, useful in the
PT   manufacture of a pharmaceutical composition for preventing cervical
PT   lesions and carcinomas.
XX
PS   Claim 1; Fig 5; 36pp; English.
XX
CC   The invention relates to a new isolated nucleotide sequence containing a
CC   papillomavirus sequence, encoding the L1 capsid protein. The activity of
CC   nucleotide sequences of the invention may be described as virucidal and
CC   immunostimulantary. The isolated nucleotide sequence is useful in a
CC   method of producing a papillomavirus protein. The papillomavirus protein
CC   encoded by the nucleotide sequence is useful in the manufacture of a
CC   pharmaceutical composition for prophylactic treatment of cervical lesions
CC   and carcinomas caused by papillomavirus. Polynucleotides of the invention
CC   may be useful in vaccines or in gene therapy. The current sequence
CC   represents the HPV 16 L1 capsid protein gene SA-L1-NLS (South African
CC   isolate)
XX
SQ   Sequence 1452 BP; 458 A; 271 C; 281 G; 442 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 10;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 3
ACC47505/c
ID   ACC47505 standard; DNA; 1452 BP.
XX
AC   ACC47505;
XX
DT   27-JUN-2003  (first entry)
XX
DE   HPV 16 L1 capsid protein gene SAopt-L1-NLS.
XX
KW   L1 capsid protein; HPV 16; virucide; immunostimulant; gene therapy;
KW   vaccine; cervical lesion; carcinoma; gene; ds.
XX
OS   Human papillomavirus.
XX
PN   WO2003018623-A2.
XX
PD   06-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-IB003531.
XX
PR   31-AUG-2001; 2001ZA-00007228.
XX
PA   (UYCA-) UNIV CAPE TOWN.
XX
PI   Varsani AD,  Rybicki EP,  Williamson A;
XX
DR   WPI; 2003-290048/28.
XX
PT   New nucleotide sequence encoding papillomavirus protein, useful in the
PT   manufacture of a pharmaceutical composition for preventing cervical
PT   lesions and carcinomas.
XX
PS   Claim 1; Fig 7; 36pp; English.
XX
CC   The invention relates to a new isolated nucleotide sequence containing a
CC   papillomavirus sequence, encoding the L1 capsid protein. The activity of
CC   nucleotide sequences of the invention may be described as virucidal and
CC   immunostimulantary. The isolated nucleotide sequence is useful in a
CC   method of producing a papillomavirus protein. The papillomavirus protein
CC   encoded by the nucleotide sequence is useful in the manufacture of a
CC   pharmaceutical composition for prophylactic treatment of cervical lesions
CC   and carcinomas caused by papillomavirus. Polynucleotides of the invention
CC   may be useful in vaccines or in gene therapy. The current sequence
CC   represents the HPV 16 L1 capsid protein gene SAopt-L1-NLS (Optimised
CC   South African isolate)
XX
SQ   Sequence 1452 BP; 459 A; 271 C; 280 G; 442 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 10;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 4
AAX89755/c
ID   AAX89755 standard; DNA; 1484 BP.
XX
AC   AAX89755;
XX
DT   27-AUG-2003  (revised)
DT   12-OCT-1999  (first entry)
XX
DE   Probe sequence for HPV 16 L1.
XX
KW   human papilloma virus; infection; gene expression; probe; detection;
```

```
KW   assay; cancer; virus; HPV; ss.
XX
OS   Synthetic.
OS   Human papillomavirus.
XX
PN   WO9929890-A2.
XX
PD   17-JUN-1999.
XX
PF   11-DEC-1998;   98WO-US026447.
XX
PR   12-DEC-1997;   97US-0069426P.
PR   05-JAN-1998;   98US-0070486P.
PR   17-APR-1998;   98US-0082167P.
XX
PA   (DIGE-) DIGENE CORP.
XX
PI   Lorincz AT;
XX
DR   WPI; 1999-443850/37.
XX
PT   New method for assessing Human Papilloma Virus (HPV) infection by
PT   comparison of gene expression levels.
XX
PS   Disclosure; Fig 4; 35pp; English.
XX
CC   This nucleotide probe is specific for the HPV16 Human Papilloma Virus
CC   (HPV) gene. The degree of HPV infection can be assessed, by measuring the
CC   levels of expression of genes involved in the diseased state, and
CC   comparing the expression to each other or to reference genes. (Updated on
CC   27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 1484 BP; 481 A; 285 C; 277 G; 441 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1484;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        890 GCATCAGAGGTAACCATAGAACCACTAGG 862


RESULT 5
AAD01237/c
ID   AAD01237 standard; DNA; 1494 BP.
XX
AC   AAD01237;
XX
DT   04-OCT-2000  (first entry)
XX
DE   Chimeric biotin-binding human papillomavirus mutant L1 protein-168 DNA.
XX
KW   Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;
KW   cytostatic; antiviral; gene therapy; vaccine; capsomere; VLP;
KW   virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL;
KW   interleukin; chemotherapeutic agent; radioactive agent; mutant; ds.
XX
OS   Human papillomavirus type 16.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1494
FT                   /*tag=  a
FT                   /product= "Chimeric protein 168 containing human
FT                   papillomavirus 16 mutant L1 protein fused to biotin-
FT                   binding peptide at the C-terminal"
FT   misc_feature    1450. .1494
FT                   /*tag=  b
FT                   /note= "Biotin-binding peptide DNA"
XX
PN   WO200031128-A1.
XX
PD   02-JUN-2000.
XX
PF   22-NOV-1999;   99WO-US027555.
XX
PR   23-NOV-1998;   98US-0109510P.
PR   06-OCT-1999;   99US-00413611.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Mueller M,  Kast WM,  Nieland JD,  Velders MP;
XX
DR   WPI; 2000-400041/34.
DR   P-PSDB; AAY71464.
XX
PT   Chimeric protein comprising a papillomavirus L1 or L2 protein and a
PT   biotin-binding polypeptide, useful for delivering substances such as
PT   proteins, nucleic acids and lipids into cells, particularly
PT   papillomavirus infected cells.
XX
PS   Example 1; Page 15-18; 27pp; English.
XX
CC   The patent discloses a chimeric protein comprising papillomavirus L1 or
CC   L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus or
CC   virus-like particle (VLP) comprising the chimeric protein is used for
CC   delivering a wide variety of biotinylated compounds e.g. proteins,
CC   nucleic acids and lipids into cells, particularly papillomavirus infected
CC   cells. The chimeric protein may also be used as a vaccine when the
CC   biotinylated substance is a viral antigen e.g. papillomavirus E2 or E7
CC   proteins. It may be useful for treating tumours or other papillomavirus-
CC   related lesions when the substance is a cytotoxin, chemotherapeutic
CC   agent, radioactive agent, or a gene encoding a cytokine or interleukin.
CC   The present sequence is a DNA encoding a chimeric protein 168 consisting
CC   of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotin-
CC   binding peptide at the C-terminus. The L1 protein was derived from the
CC   wild-type sequence by deleting the amino acid Cys428. The modification
CC   was done to prevent assembly of VLPs while allowing the production of
CC   capsomeres at high efficiencies
XX
SQ   Sequence 1494 BP; 462 A; 291 C; 292 G; 449 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1494;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 6
AAD01238/c
ID   AAD01238 standard; DNA; 1500 BP.
XX
AC   AAD01238;
XX
DT   04-OCT-2000  (first entry)
XX
DE   Chimeric biotin-binding human papillomavirus mutant L1 protein-169 DNA.
XX
KW   Human papillomavirus; HPV; L1 protein; L2 protein; biotin; chimeric;
KW   cytostatic; antiviral; gene therapy; vaccine; capsomere; VLP;
KW   virus-like particle; viral antigen; tumour; cytotoxin; cytokine; IL;
KW   interleukin; chemotherapeutic agent; radioactive agent; mutant; ds.
XX
OS   Human papillomavirus type 16.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1500
FT                   /*tag=  a
FT                   /product= "Chimeric protein 169 containing human
```

```
FT                  papillomavirus 16 mutant L1 protein fused to biotin-
FT                  binding peptide at the C-terminal"
FT   misc_feature   1450. .1500
FT                  /*tag= b
FT                  /note= "Biotin-binding peptide DNA"
XX
PN   WO200031128-A1.
XX
PD   02-JUN-2000.
XX
PF   22-NOV-1999;   99WO-US027555.
XX
PR   23-NOV-1998;   98US-0109510P.
PR   06-OCT-1999;   99US-00413611.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Mueller M, Kast WM, Nieland JD, Velders MP;
XX
DR   WPI; 2000-400041/34.
DR   P-PSDB; AAY71465.
XX
PT   Chimeric protein comprising a papillomavirus L1 or L2 protein and a
PT   biotin-binding polypeptide, useful for delivering substances such as
PT   proteins, nucleic acids and lipids into cells, particularly
PT   papillomavirus infected cells.
XX
PS   Example 1; Page 20-23; 27pp; English.
XX
CC   The patent discloses a chimeric protein comprising papillomavirus L1 or
CC   L2 protein and a biotin-binding polypeptide. Capsomere, papillomavirus or
CC   virus-like particle (VLP) comprising the chimeric protein is used for
CC   delivering a wide variety of biotinylated compounds e.g. proteins,
CC   nucleic acids and lipids into cells, particularly papillomavirus infected
CC   cells. The chimeric protein may also be used as a vaccine when the
CC   biotinylated substance is a viral antigen e.g. papillomavirus E2 or E7
CC   proteins. It may be useful for treating tumours or other papillomavirus-
CC   related lesions when the substance is a cytotoxin, chemotherapeutic
CC   agent, radioactive agent, or a gene encoding a cytokine or interleukin.
CC   The present sequence is a DNA encoding a chimeric protein 169 consisting
CC   of human papillomavirus 16 (HPV-16) mutant L1 protein fused to a biotin-
CC   binding peptide at the C-terminus. The L1 protein was derived from the
CC   wild-type sequence by deleting the amino acid Cys428. The modification
CC   was done to prevent assembly of VLPs while allowing the production of
CC   capsomeres at high efficiencies
XX
SQ   Sequence 1500 BP; 467 A; 291 C; 295 G; 447 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1500;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 7
AAQ47167/c
ID   AAQ47167 standard; DNA; 1517 BP.
XX
AC   AAQ47167;
XX
DT   25-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   21-JAN-1994  (first entry)
XX
DE   HPV1 L1 ORF.
XX
KW   L1; capsid protein; bovine; human; papillomavirus; baculovirus;
KW   transfer vector; promoter; capsid protein; transformation; vaccine;
KW   neutralising antibody; vertebrate; ss.
XX
OS   Human papillomavirus.
XX
PN   USN8032869-N.
XX
PD   15-JUL-1993.
XX
PF   16-MAR-1993;   93US-00032869.
XX
PR   03-SEP-1992;   92US-00941371.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Lowy DR, Schiller JT, Kirnbauer R;
XX
DR   WPI; 1993-249995/31.
DR   P-PSDB; AAR38808.
XX
PT   Recombinant papilloma virus capsid proteins - for vaccines against
PT   papilloma virus and for diagnosis of virus infection.
XX
PS   Example 1; Page 35-37; 45pp; English.
XX
CC   The sequences given in AAQ47166-67 encode the L1 capsid proteins from
CC   bovine and human papillomavirus respectively. These sequences may be
CC   inserted into a baculovirus transfer vector and operatively expressed by
CC   a promoter of the vector, and the capsid protein produced by transformed
CC   cells. The capsid protiens may be used in vaccines to induce high-titre
CC   neutralising antibody response in vertebrates. (Note: Revised entry
CC   submitted to correct the patent number format of US Government-owned NTIS
CC   applications to prevent clashes with ongoing US granted patent numbers.
CC   For further information please visit the Derwent web site at
CC   www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 8
AAQ47166/c
ID   AAQ47166 standard; DNA; 1517 BP.
XX
AC   AAQ47166;
XX
DT   25-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   21-JAN-1994  (first entry)
XX
DE   BPV1 L1 ORF.
XX
KW   L1; capsid protein; bovine; human; papillomavirus; baculovirus;
KW   transfer vector; promoter; capsid protein; transformation; vaccine;
KW   neutralising antibody; vertebrate; ss.
XX
OS   Bovine papillomavirus.
XX
PN   USN8032869-N.
XX
PD   15-JUL-1993.
XX
PF   16-MAR-1993;   93US-00032869.
XX
PR   03-SEP-1992;   92US-00941371.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
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PI   Lowy DR,  Schiller JT,  Kirnbauer R;
XX
DR   WPI; 1993-249995/31.
DR   P-PSDB; AAR38807.
XX
PT   Recombinant papilloma virus capsid proteins - for vaccines against
PT   papilloma virus and for diagnosis of virus infection.
XX
PS   Example 1; Page 32-34; 45pp; English.
XX
CC   The sequences given in AAQ47166-67 encode the L1 capsid proteins from
CC   bovine and human papillomavirus respectively. These sequences may be
CC   inserted into a baculovirus transfer vector and operatively expressed by
CC   a promoter of the vector, and the capsid protein produced by transformed
CC   cells. The capsid protiens may be used in vaccines to induce high-titre
CC   neutralising antibody response in vertebrates. (Note: Revised entry
CC   submitted to correct the patent number format of US Government-owned NTIS
CC   applications to prevent clashes with ongoing US granted patent numbers.
CC   For further information please visit the Derwent web site at
CC   www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 9
AAV09856/c
ID   AAV09856 standard; DNA; 1517 BP.
XX
AC   AAV09856;
XX
DT   26-MAY-1998  (first entry)
XX
DE   HPV16 recombinant L1 capsid protein DNA.
XX
KW   Capsid protein; L1; HPV16; vaccine; prevention; treatment; self-assembly;
KW   viral protein; capsomer; capsid; antigenic epitope; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1517
FT                   /*tag=  a
FT                   /product= "L1"
FT                   /note= "partial recombinant capsid protein sequence"
XX
PN   US5716620-A.
XX
PD   10-FEB-1998.
XX
PF   07-JUN-1995;   95US-00475783.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kirnbauer R,  Lowy DR,  Schiller JT;
XX
DR   WPI; 1998-158363/14.
DR   P-PSDB; AAW39904.
XX
PT   Vaccine against human papilloma virus - comprises HPV16 L1 polypeptide.
XX
PS   Claim 2; Col 21-24; 20pp; English.
XX
CC   This sequence encodes a recombinant L1 capsid protein from Human
CC   Papillomavirus strain 16 (HPV16). This recombinant form of viral protein
CC   is capable of self-assembly into capsomer structures and viral capsids
CC   that comprise conformational antigenic epitopes can be used as a vaccine
CC   for the prevention or treatment of papillomavirus infections in
CC   vertebrates. The vaccine comprises a unit dose of a composition
CC   containing a self assembled HPV16 with at least 1 papillomavirus L1
CC   conformational epitope
XX
SQ   Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 10
AAV09855/c
ID   AAV09855 standard; DNA; 1517 BP.
XX
AC   AAV09855;
XX
DT   26-MAY-1998  (first entry)
XX
DE   HPV16 L1 capsid protein DNA.
XX
KW   Capsid protein; L1; HPV16; vaccine; prevention; treatment; self-assembly;
KW   viral protein; capsomer; capsid; antigenic epitope; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1517
FT                   /*tag=  a
FT                   /product= "L1"
FT                   /note= "partial capsid protein sequence"
XX
PN   US5716620-A.
XX
PD   10-FEB-1998.
XX
PF   07-JUN-1995;   95US-00475783.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kirnbauer R,  Lowy DR,  Schiller JT;
XX
DR   WPI; 1998-158363/14.
DR   P-PSDB; AAW39903.
XX
PT   Vaccine against human papilloma virus - comprises HPV16 L1 polypeptide.
XX
PS   Disclosure; Col 17-20; 20pp; English.
XX
CC   This sequence encodes the L1 capsid protein from Human Papillomavirus
CC   strain 16 (HPV16). A recombinant form of this viral protein which is
CC   capable of self-assembly into capsomer structures and viral capsids that
CC   comprise conformational antigenic epitopes can be used as a vaccine for
CC   the prevention or treatment of papillomavirus infections in vertebrates.
CC   The vaccine comprises a unit dose of a composition containing a self
CC   assembled HPV16 with at least 1 papillomavirus L1 conformational epitope
XX
SQ   Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
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```
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 11
AAV25818/c
ID   AAV25818 standard; DNA; 1517 BP.
XX
AC   AAV25818;
XX
DT   10-JUL-1998  (first entry)
XX
DE   Human papillomavirus proto-type HPV 16 L1 genome 5637-7155.
XX
KW   Human papillomavirus; HPV 16; L1 gene; immunisation; capsid;
KW   conformational epitope; vaccine; sequelae; vertebrate; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. :1517
FT                   /*tag=  a
FT                   /product= "HPV 16 L1 proto-type"
FT                   /note= "no stop codon given"
XX
PN   US5744142-A.
XX
PD   28-APR-1998.
XX
PF   07-JUN-1995;   95US-00475782.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Schiller JT,  Kirnbauer R,  Lowy DR;
XX
DR   WPI; 1998-271010/24.
DR   P-PSDB; AAW53487.
XX
PT   Immunisation of mammals and humans against papillomavirus infection -
PT   comprises administering recombinant self-assembled capsid proteins
PT   containing conformational epitopes.
XX
PS   Disclosure; Col 17-20; 20pp; English.
XX
CC   The present sequence represents the human papillomavirus proto-type HPV
CC   16 L1 genome 5637-7155, from the present invention. The present invention
CC   describes the immunisation of a host mammal against a papillomavirus
CC   comprising administering to the host, according to an immunising
CC   schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)
CC   containing at least 1 papillomavirus L1 conformational epitope. The
CC   papillomavirus L1 conformational epitopes are produced by letting a
CC   genetic construct comprising a papillomavirus L1 gene direct recombinant
CC   expression of the conformational epitope in a transformed eukaryotic host
CC   cell by self-assembly of papillomavirus capsids containing a L1
CC   polypeptide having an amino acid sequence encoded by the nucleic acid
CC   sequence given in the specification (see AAV25817). (I) are useful for
CC   the diagnosis of and as vaccines for the prevention of papillomavirus
CC   infections and their benign and malignant sequelae in vertebrates.
CC   Recombinant conformed papillomavirus proteins are provided which can be
CC   used to produce renewable papillomavirus reagents of any selected species
CC   and type in cell culture. The self-assembled recombinant L1 capsid
CC   protein has the efficacy of intact papillomavirus particles to induce
CC   high levels of neutralising antiserum, in contrast to prior art L1
CC   protein extracted from recombinant bacteria or denatured virions
XX
SQ   Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

  Query Match           83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 12
AAV25817/c
ID   AAV25817 standard; DNA; 1517 BP.
XX
AC   AAV25817;
XX
DT   10-JUL-1998  (first entry)
XX
DE   Human papillomavirus wild-type HPV 16 L1 conformational epitope gene.
XX
KW   Human papillomavirus; HPV 16; L1 gene; immunisation; capsid;
KW   conformational epitope; vaccine; sequelae; vertebrate; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "HPV 16 L1 conformational epitope"
FT                   /note= "no stop codon given"
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PN   US5744142-A.
XX
PD   28-APR-1998.
XX
PF   07-JUN-1995;   95US-00475782.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Schiller JT,  Kirnbauer R,  Lowy DR;
XX
DR   WPI; 1998-271010/24.
DR   P-PSDB; AAW53486.
XX
PT   Immunisation of mammals and humans against papillomavirus infection -
PT   comprises administering recombinant self-assembled capsid proteins
PT   containing conformational epitopes.
XX
PS   Claim 1; Col 21-24; 20pp; English.
XX
CC   The present sequence encodes the human papillomavirus HPV 16 L1
CC   conformational epitope, from the present invention. The present invention
CC   describes the immunisation of a host mammal against a papillomavirus
CC   comprising administering to the host, according to an immunising
CC   schedule, a self-assembled Human Papilloma Virus (HPV16) capsid (I)
CC   containing at least 1 papillomavirus L1 conformational epitope. The
CC   papillomavirus L1 conformational epitopes are produced by letting a
CC   genetic construct comprising a papillomavirus L1 gene direct recombinant
CC   expression of the conformational epitope in a transformed eukaryotic host
CC   cell by self-assembly of papillomavirus capsids containing a L1
CC   polypeptide having an amino acid sequence encoded by the nucleic acid
CC   sequence given in the specification (present sequence). (I) are useful
CC   for the diagnosis of and as vaccines for the prevention of papillomavirus
CC   infections and their benign and malignant sequelae in vertebrates.
CC   Recombinant conformed papillomavirus proteins are provided which can be
CC   used to produce renewable papillomavirus reagents of any selected species
CC   and type in cell culture. The self-assembled recombinant L1 capsid
CC   protein has the efficacy of intact papillomavirus particles to induce
CC   high levels of neutralising antiserum, in contrast to prior art L1
CC   protein extracted from recombinant bacteria or denatured virions
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XX
SQ   Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 13
AAV12161/c
ID   AAV12161 standard; DNA; 1517 BP.
XX
AC   AAV12161;
XX
DT   05-MAY-1998  (first entry)
XX
DE   Human papillomavirus wild-type L1 gene.
XX
KW   Human; papillomavirus; bovine; L1 conformational protein; antibody;
KW   detection; diagnosis; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "L1"
FT                   /note= "no stop codon given"
XX
PN   US5709996-A.
XX
PD   20-JAN-1998.
XX
PF   07-JUN-1995;   95US-00472673.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Schiller JT,  Kirnbauer R,  Lowy DR;
XX
DR   WPI; 1998-109811/10.
DR   P-PSDB; AAW44142.
XX
PT   Assay for papilloma virus - using antibody directed against recombinant
PT   L1 polypeptide.
XX
PS   Claim 1; Col 21-24; 34pp; English.
XX
CC   An method has been developed for detecting papilloma virus in a specimen
CC   from a mammal. The method comprises contacting the sample with an
CC   antibody and detecting any antibody binding. The antibody is a polyclonal
CC   or monoclonal antibody produced by transforming a eukaryotic host cell
CC   with a genetic construct containing a papillomavirus L1 gene so that the
CC   cell expresses self-assembled papillomavirus-like particles containing at
CC   least 1 papillomavirus L1 conformational epitope. The present sequence
CC   encodes wild-type human papillomavirus L1 polypeptide. The method is for
CC   the diagnosis of papillomavirus infections in mammals
XX
SQ   Sequence 1517 BP; 487 A; 291 C; 286 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 14
AAV12162/c
ID   AAV12162 standard; DNA; 1517 BP.
XX
AC   AAV12162;
XX
DT   05-MAY-1998  (first entry)
XX
DE   Human papillomavirus prototype L1 gene.
XX
KW   Human; papillomavirus; bovine; L1 conformational protein; antibody;
KW   detection; diagnosis; ss.
XX
OS   Human papillomavirus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1517
FT                   /*tag=  a
FT                   /product= "L1"
FT                   /note= "no stop codon given"
XX
PN   US5709996-A.
XX
PD   20-JAN-1998.
XX
PF   07-JUN-1995;   95US-00472673.
XX
PR   03-SEP-1992;   92US-00941371.
PR   16-MAR-1993;   93US-00032869.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Schiller JT,  Kirnbauer R,  Lowy DR;
XX
DR   WPI; 1998-109811/10.
DR   P-PSDB; AAW44143.
XX
PT   Assay for papilloma virus - using antibody directed against recombinant
PT   L1 polypeptide.
XX
PS   Disclosure; Col 17-20; 34pp; English.
XX
CC   An method has been developed for detecting papilloma virus in a specimen
CC   from a mammal. The method comprises contacting the sample with an
CC   antibody and detecting any antibody binding. The antibody is a polyclonal
CC   or monoclonal antibody produced by transforming a eukaryotic host cell
CC   with a genetic construct containing a papillomavirus L1 gene so that the
CC   cell expresses self-assembled papillomavirus-like particles containing at
CC   least 1 papillomavirus L1 conformational epitope. The present sequence
CC   encodes prototype human papillomavirus L1 polypeptide. The method is for
CC   the diagnosis of papillomavirus infections in mammals
XX
SQ   Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.18;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 15
AAV23923/c
ID   AAV23923 standard; DNA; 1517 BP.
XX
AC   AAV23923;
XX
DT   17-OCT-2003  (revised)
DT   10-AUG-1998  (first entry)
```

XX
DE HPV16 L1 gene #1.
XX
KW Human papillomavirus 16; HPV17; L1 gene; infection; antibody detection;
KW ss.
XX
OS Human papillomavirus type 16.
XX
FH Key Location/Qualifiers
FT CDS 1. .1515
FT /*tag= a
FT /note= "no stop codon given"
XX
PN US5756284-A.
XX
PD 26-MAY-1998.
XX
PF 07-JUN-1995; 95US-00472672.
XX
PR 03-SEP-1992; 92US-00941371.
PR 16-MAR-1993; 93US-00032869.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kirnbauer R, Lowy DR, Schiller JT;
XX
DR WPI; 1998-321522/28.
DR P-PSDB; AAW54034.
XX
PT Assay for antibodies to papilloma virus - using self-assembled
PT papillomavirus-like particles comprising L1 polypeptide.
XX
PS Disclosure; Col 17-20; 21pp; English.
XX
CC This sequence encodes the human papillomavirus 16 (HPV16) L1 gene
CC protein. The protein can be used in the method of the invention for
CC detecting antibodies to a papilloma virus in a sample from a mammal. The
CC method comprises: (a) providing self-assembled papillomavirus-like
CC particles comprising a L1 polypeptide, where the self-assembled
CC papillomavirus-like particles comprise at least one L1 conformational
CC epitope and are produced by permitting a genetic construct comprising a
CC papillomavirus L1 gene to direct recombinant expression in a transformed
CC eukaryotic host cell; (b) contacting the sample with the self-assembled
CC papillomavirus-like particles; and (c) detecting any antibody binding to
CC the self-assembled papillomavirus-like particles. The method can be used
CC for detecting antibodies to HPV16 as an indication of infection. (Updated
CC on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1517 BP; 487 A; 293 C; 284 G; 453 T; 0 U; 0 Other;

Query Match 83.4%; Score 24.2; DB 2; Length 1517;
Best Local Similarity 89.7%; Pred. No. 0.18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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Search completed: March 5, 2006, 22:12:08
Job time : 381.5 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:59:29 ; Search time 3168 Seconds
(without alignments)
428.291 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	20	69.0	798	10	BX227374	BX227374 Danio rer
	3	20	69.0	828	10	BX216514	BX216514 Danio rer
	4	19.8	68.3	191	1	AJ760626	AJ760626 AJ760626
	5	19.8	68.3	280	1	AJ763893	AJ763893 AJ763893
	6	19.6	67.6	486	9	AZ221755	AZ221755 RPCI-23-5
c	7	19.6	67.6	537	1	AU243490	AU243490 AU243490
	8	19.6	67.6	552	9	AZ256958	AZ256958 RPCI-23-1
	9	19.6	67.6	601	11	DE105340	DE105340 Oryzias l
c	10	19.6	67.6	613	7	CV504457	CV504457 71003.1 M
	11	19.6	67.6	765	7	CK260235	CK260235 EST706313
	12	19.6	67.6	790	7	CK260232	CK260232 EST706310
	13	19.6	67.6	803	11	DE114072	DE114072 Oryzias l
	14	19.6	67.6	838	11	CR099508	CR099508 Forward s
	15	19.6	67.6	990	10	CL110457	CL110457 ISB1-53J1
	16	19.4	66.9	425	9	BZ161634	BZ161634 CH230-388
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c	19	19.4	66.9	503	3	BM530649	BM530649 fx47c05.y
c	20	19.4	66.9	591	6	CA875703	CA875703 K0943A01-
	21	19.4	66.9	670	1	AJ730032	AJ730032 AJ730032
c	22	19.4	66.9	689	9	AZ501268	AZ501268 1M0340K04
c	23	19.4	66.9	1027	2	BG745404	BG745404 602723750
c	24	19.4	66.9	1307	3	BI457107	BI457107 603185348
c	25	19.2	66.2	496	1	AW321749	AW321749 uo38c03.y
	26	19.2	66.2	639	10	CZ735950	CZ735950 OC__Ba007
	27	19.2	66.2	692	10	CZ815849	CZ815849 OC__Ba019
c	28	19.2	66.2	742	6	CF347434	CF347434 AGENCOURT
	29	19.2	66.2	752	10	CZ864166	CZ864166 OC__Ba025
	30	19.2	66.2	795	10	CZ783180	CZ783180 OC__Ba014
c	31	19.2	66.2	899	10	CG768184	CG768184 TcB48.4_B
c	32	19.2	66.2	2122	4	AK031646	AK031646 Mus muscu
	33	19	65.5	361	9	B87751	B87751 RPCI11-30F1
	34	19	65.5	744	10	BX208090	BX208090 Danio rer
	35	19	65.5	763	9	CC903234	CC903234 t006i15ba
	36	19	65.5	771	3	BQ158020	BQ158020 NF015B02P
c	37	19	65.5	775	5	BW938474	BW938474 BW938474
c	38	19	65.5	835	10	BX213865	BX213865 Danio rer
	39	19	65.5	864	7	CK290626	CK290626 EST753340
	40	19	65.5	902	7	CR575491	CR575491 CR575491
	41	19	65.5	908	8	CX469660	CX469660 JGI_XZG39
	42	19	65.5	908	10	CZ507804	CZ507804 GMW2-60H1
c	43	19	65.5	919	10	CZ505564	CZ505564 GMW2-11A1
	44	19	65.5	925	10	CZ500920	CZ500920 GMW2-10G2
c	45	19	65.5	1062	6	CA495435	CA495435 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS DN408692 589 bp mRNA linear EST 07-MAR-2005
DEFINITION LIB4007-010-Q6-K1-B3 LIB4007 Canis familiaris cDNA clone CLN9364981, mRNA sequence.
ACCESSION DN408692
VERSION DN408692.1 GI:60589913
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 589)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
FEATURES Location/Qualifiers
source 1. .589
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
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/lab_host="DH10B"
/clone_lib="LIB4007"
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ORIGIN

Query Match 69.0%; Score 20; DB 8; Length 589;
Best Local Similarity 82.1%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAG 28
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Db        111 GCGTCTTATCTTACCATATAGCCACTAG 138
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RESULT 2
BX227374

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LOCUS       BX227374                798 bp    DNA     linear   GSS 29-JAN-2003
DEFINITION  Danio rerio genomic clone DKEY-277E24, genomic survey sequence.
ACCESSION   BX227374
VERSION     BX227374.1  GI:28061524
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 277E24. 277E24
            is part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAG 28
              ||||||| | ||||||  ||||||| ||
Db        496 GCGTCAGTGCTTACCACTGAGCCACCAG 523


RESULT 3
BX216514
LOCUS       BX216514                828 bp    DNA     linear   GSS 13-MAR-2003
DEFINITION  Danio rerio genomic clone DKEY-247D6, genomic survey sequence.
ACCESSION   BX216514
VERSION     BX216514.1  GI:28048400
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the T7 end of BAC 247D6. 247D6 is
            part of the Daniokey BAC Library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1. .828
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                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"
ORIGIN

  Query Match             69.0%;  Score 20;  DB 10;  Length 828;
  Best Local Similarity   82.1%;  Pred. No. 2.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAG 28
              ||||||| | ||||||  ||||||| ||
Db        568 GCGTCAGTGCTTACCACTGAGCCACCAG 595


RESULT 4
AJ760626
LOCUS       AJ760626                191 bp    mRNA    linear   EST 03-JUN-2005
DEFINITION  AJ760626 G00005 Gerbera hybrid cv. 'Terra Regina' cDNA clone
            G0000500010E12F1, mRNA sequence.
ACCESSION   AJ760626
VERSION     AJ760626.1  GI:62941681
KEYWORDS    EST.
SOURCE      Gerbera hybrid cv. 'Terra Regina'
  ORGANISM  Gerbera hybrid cv. 'Terra Regina'
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Mutisioideae;
            Mutisieae; Gerbera.
REFERENCE   1  (bases 1 to 191)
  AUTHORS   Laitinen,R.A., Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,
            Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and
            Elomaa,P.
  TITLE     Analysis of the floral transcriptome uncovers new regulators of
            organ determination and gene families related to flower organ
            differentiation in Gerbera hybrida (Asteraceae)
  JOURNAL   Genome Res. 15 (4), 475-486 (2005)
   PUBMED   15781570
COMMENT     Contact: Alatalo ER
            Institute of Biotechnology
            Viikinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.
FEATURES             Location/Qualifiers
     source          1. .191
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ORIGIN

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  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCATAGAGCCACT 26
              ||||||||| |||||||||| ||
Db         32 TCAGAGGTTGCCATAGAGCCTCT 54


RESULT 5
AJ763893
LOCUS       AJ763893                280 bp    mRNA    linear   EST 03-JUN-2005
DEFINITION  AJ763893 G00007 Gerbera hybrid cv. 'Terra Regina' cDNA clone
            G0000700010E06F1, mRNA sequence.
ACCESSION   AJ763893
VERSION     AJ763893.1  GI:58327558
KEYWORDS    EST.
SOURCE      Gerbera hybrid cv. 'Terra Regina'
  ORGANISM  Gerbera hybrid cv. 'Terra Regina'
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; campanulids; Asterales; Asteraceae; Mutisioideae;
            Mutisieae; Gerbera.
REFERENCE   1  (bases 1 to 280)
  AUTHORS   Laitinen,R.A., Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,
            Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and
            Elomaa,P.
  TITLE     Analysis of the floral transcriptome uncovers new regulators of
            organ determination and gene families related to flower organ
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            differentiation in Gerbera hybrida (Asteraceae)
  JOURNAL   Genome Res. 15 (4), 475-486 (2005)
   PUBMED   15781570
COMMENT     Contact: Alatalo ER
            Institute of Biotechnology
            Viikinkaari 9, P.O. Box 56, 00014 University of Helsinki, FINLAND.
FEATURES             Location/Qualifiers
     source          1. .280
                     /organism="Gerbera hybrid cv. 'Terra Regina'"
                     /mol_type="mRNA"
                     /cultivar="Terra Regina"
                     /db_xref="taxon:226891"
                     /clone="G0000700010E06F1"
                     /tissue_type="early petal"
                     /dev_stage="1-4"
                     /clone_lib="G00007"
ORIGIN

  Query Match             68.3%;  Score 19.8;  DB 1;  Length 280;
  Best Local Similarity   91.3%;  Pred. No. 2.8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCATAGAGCCACT 26
              ||||||||| |||||||||| ||
Db         45 TCAGAGGTTGCCATAGAGCCTCT 67


RESULT 6
AZ221755
LOCUS       AZ221755                 486 bp    DNA     linear   GSS 14-JUN-2000
DEFINITION  RPCI-23-50C11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-50C11,
            genomic survey sequence.
ACCESSION   AZ221755
VERSION     AZ221755.1  GI:8529804
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-50C11.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 50  row: C  column: 11
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-50C11"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 9;  Length 486;
  Best Local Similarity   84.6%;  Pred. No. 3.9e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              || | |||| |||||| |||||||||
Db        140 GCTTTAGAGATTACCACAGAGCCACT 165


RESULT 7
AU243490/c
LOCUS       AU243490                 537 bp    mRNA    linear   EST 15-JAN-2002
DEFINITION  AU243490 Medaka eye cDNA library (SNK01) Oryzias latipes cDNA clone
            NGY33.03h, mRNA sequence.
ACCESSION   AU243490
VERSION     AU243490.1  GI:18156069
KEYWORDS    EST.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1  (bases 1 to 537)
  AUTHORS   Sanaka,E., Hori,H., Naruse,K., Mitani,H. and Tanaka,M.
  TITLE     Medaka EST analysis
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Emi Sanaka
            Department of Biological Sciences
            Graduate School of Science, Nagoya University
            Furo-cho, Chikusa-ku, Nagoya 464-8602, Japan
            Tel: 81-52-789-2973
            Fax: 81-52-789-2974
            Email: sanaka@bio.nagoya-u.ac.jp
            This clone was isolated from Medaka eye cDNA library (SNK01) 5'end.
FEATURES             Location/Qualifiers
     source          1. .537
                     /organism="Oryzias latipes"
                     /mol_type="mRNA"
                     /strain="wild type"
                     /db_xref="taxon:8090"
                     /clone="NGY33.03h"
                     /tissue_type="eye"
                     /dev_stage="adult"
                     /clone_lib="Medaka eye cDNA library (SNK01)"
                     /note="Wild samples from Okayama Pref.(Southern part of
                     Japan)"
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 1;  Length 537;
  Best Local Similarity   84.6%;  Pred. No. 4e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              | ||||| |||| |||||||| ||||
Db        126 GAGTCAGTGGTTTCCATAGAGACACT 101


RESULT 8
AZ256958
LOCUS       AZ256958                 552 bp    DNA     linear   GSS 26-JUL-2000
DEFINITION  RPCI-23-149O3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-149O3,
            genomic survey sequence.
ACCESSION   AZ256958
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VERSION     AZ256958.1  GI:9461222
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-149O3.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 149  row: O  column: 3
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-149O3"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).   "
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 9;  Length 552;
  Best Local Similarity   84.6%;  Pred. No. 4e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              || | |||| |||||| |||||||||
Db        187 GCTTTAGAGATTACCACAGAGCCACT 212


RESULT 9
DE105340
LOCUS       DE105340                601 bp    DNA     linear   GSS 02-AUG-2005
DEFINITION  Oryzias latipes DNA, forward end of BAC clone: Md0145B09, genomic
            survey sequence.
ACCESSION   DE105340
VERSION     DE105340.1  GI:71637508
KEYWORDS    GSS.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1
  AUTHORS   Shimizu,N., Asakawa,S., Shimizu,A. and Sasaki,T.
  TITLE     The BAC end sequence of Oryzias latipes
  JOURNAL   Published Only in Database (2005)
REFERENCE   2  (bases 1 to 601)
  AUTHORS   Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
            Tokyo, 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Oryzias latipes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:8090"
                     /clone="Md0145B09"
                     /clone_lib="Medaka HdrR BAC library"
                     /note="This sequence is forward end of BAC clone
                     Md0145B09."
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 11;  Length 601;
  Best Local Similarity   84.6%;  Pred. No. 4.1e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              | ||||| |||| |||||||| ||||
Db        177 GAGTCAGTGGTTTCCATAGAGACACT 202


RESULT 10
CV504457/c
LOCUS       CV504457                613 bp    mRNA    linear   EST 04-OCT-2004
DEFINITION  71003.1 Mixed Floral Solanum tuberosum cDNA clone 71003 5', mRNA
            sequence.
ACCESSION   CV504457
VERSION     CV504457.1  GI:53786814
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 613)
  AUTHORS   Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De
            Koeyer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.
  TITLE     Generation of ESTs from a normalized developing floral bud library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Barry Flinn
            The Canadian Potato Genome Project - BioAtlantech
            921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
            Email: bflinn@bioatlantech.nb.ca
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .613
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Shepody"
                     /db_xref="taxon:4113"
                     /clone="71003"
                     /tissue_type="Floral buds"
                     /lab_host="XL10-Gold"
                     /clone_lib="Mixed Floral"
                     /note="Vector: pBluescript II SK(+) XR; Site_1: EcoRI;
                     Site_2: XhoI; supplier: Developmental series. Plants from
                     pathogen-free Solanum tuberosum var. Shepody, clone 1756,
                     nuclear stock were grown in a screenhouse under natural
                     conditions. Developing floral buds were harvested at
                     various sizes up to opening and pooled. RNA was isolated
                     and used for library construction. A normalized library
                     was constructed following a modified protocol of Bonaldo
                     et al. (1996. Genome Research 6: 791-806)."
ORIGIN
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  Query Match             67.6%;  Score 19.6;  DB 7;  Length 613;
  Best Local Similarity   84.6%;  Pred. No. 4.1e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACCATAGAGCCACTAG 28
              |||||||||| |  | ||||||||||
Db        149 GTCAGAGGTTGCTTTTGAGCCACTAG 124


RESULT 11
CK260235
LOCUS       CK260235                765 bp    mRNA    linear   EST 03-AUG-2004
DEFINITION  EST706313 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAB294 3' end, mRNA sequence.
ACCESSION   CK260235
VERSION     CK260235.1  GI:39817213
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST706310 EST706311 EST706312
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from the University of Arizona Genomics
            Institute via http://genome.arizona.edu/orders/ .
            Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES             Location/Qualifiers
     source          1. .765
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POAB294"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 7;  Length 765;
  Best Local Similarity   84.6%;  Pred. No. 4.2e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACCATAGAGCCACTAG 28
              |||||||||| |  | ||||||||||
Db        669 GTCAGAGGTTGCTTTTGAGCCACTAG 694


RESULT 12
CK260232
LOCUS       CK260232                790 bp    mRNA    linear   EST 03-AUG-2004
DEFINITION  EST706310 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAB294 3' end, mRNA sequence.
ACCESSION   CK260232
VERSION     CK260232.1  GI:39817210
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 790)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST706311 EST706312 EST706313
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from the University of Arizona Genomics
            Institute via http://genome.arizona.edu/orders/ .
            Seq primer: TGT AAA ACG ACG GCC AGT.
FEATURES             Location/Qualifiers
     source          1. .790
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POAB294"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 7;  Length 790;
  Best Local Similarity   84.6%;  Pred. No. 4.3e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACCATAGAGCCACTAG 28
              |||||||||| |  | ||||||||||
Db        669 GTCAGAGGTTGCTTTTGAGCCACTAG 694
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RESULT 13
DE114072
LOCUS       DE114072                 803 bp    DNA     linear   GSS 02-AUG-2005
DEFINITION  Oryzias latipes DNA, forward end of BAC clone: Md0158G03, genomic
            survey sequence.
ACCESSION   DE114072
VERSION     DE114072.1  GI:71633484
KEYWORDS    GSS.
SOURCE      Oryzias latipes (Japanese medaka)
  ORGANISM  Oryzias latipes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
REFERENCE   1
  AUTHORS   Shimizu,N., Asakawa,S., Shimizu,A. and Sasaki,T.
  TITLE     The BAC end sequence of Oryzias latipes
  JOURNAL   Published Only in Database (2005)
REFERENCE   2  (bases 1 to 803)
  AUTHORS   Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku,
            Tokyo, 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Oryzias latipes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:8090"
                     /clone="Md0158G03"
                     /clone_lib="Medaka HdrR BAC library"
                     /note="This sequence is forward end of BAC clone
                     Md0158G03."
ORIGIN

  Query Match             67.6%;  Score 19.6;  DB 11;  Length 803;
  Best Local Similarity   84.6%;  Pred. No. 4.3e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              | ||||| |||| |||||||| ||||
Db        289 GAGTCAGTGGTTTCCATAGAGACACT 314


RESULT 14
CR099508
LOCUS       CR099508                 838 bp    DNA     linear   GSS 05-JUL-2004
DEFINITION  Forward strand read from insert in 3'HPRT insertion targeting and
            chromosome engineering clone MHPP279f02, genomic survey sequence.
ACCESSION   CR099508
VERSION     CR099508.1  GI:49846907
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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RESULT 15
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DEFINITION  ISB1-53J18_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-53J18,
            genomic survey sequence.
ACCESSION   CL110457
VERSION     CL110457.1  GI:40604092
KEYWORDS    GSS.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 75000   Std Error: 0.00
            Seq primer: T7 TAATACGACTCACTATAGGG
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            High quality sequence start: 75
            High quality sequence stop: 773.
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
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                     /clone="ISB1-53J18"
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                     /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
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ORIGIN

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  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db        755 GTAAGATGATACCATATAGCCACTAG 780


Search completed: March  5, 2006, 23:58:01
Job time : 3171 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 80.5 Seconds
(without alignments)
640.364 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	24.2	83.4	1494	3	US-09-413-611A-5	Sequence 5, Appli
c 3	24.2	83.4	1500	3	US-09-413-611A-7	Sequence 7, Appli
c 4	24.2	83.4	1517	2	US-08-032-869A-1	Sequence 1, Appli
c 5	24.2	83.4	1517	2	US-08-032-869A-2	Sequence 2, Appli
c 6	24.2	83.4	1517	2	US-08-472-673-1	Sequence 1, Appli
c 7	24.2	83.4	1517	2	US-08-472-673-2	Sequence 2, Appli
c 8	24.2	83.4	1517	2	US-08-475-782-1	Sequence 1, Appli
c 9	24.2	83.4	1517	2	US-08-475-782-2	Sequence 2, Appli
c 10	24.2	83.4	1517	2	US-08-472-678-1	Sequence 1, Appli
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c 12	24.2	83.4	1517	2	US-08-484-503-1	Sequence 1, Appli
c 13	24.2	83.4	1517	2	US-08-484-503-2	Sequence 2, Appli
c 14	24.2	83.4	1518	3	US-08-944-368A-1	Sequence 1, Appli
c 15	24.2	83.4	1518	3	US-09-820-764-1	Sequence 1, Appli
c 16	24.2	83.4	1518	3	US-09-986-118A-1	Sequence 1, Appli
c 17	24.2	83.4	1518	3	US-09-824-017-1	Sequence 1, Appli
c 18	24.2	83.4	7904	2	US-08-316-239B-1	Sequence 1, Appli
c 19	24.2	83.4	7904	2	US-08-316-239B-2	Sequence 2, Appli
c 20	24.2	83.4	7904	2	US-08-410-005-1	Sequence 1, Appli
c 21	24.2	83.4	7904	3	US-08-929-140-1	Sequence 1, Appli
c 22	24.2	83.4	7904	3	US-09-560-579A-1	Sequence 1, Appli
c 23	24.2	83.4	7917	2	US-08-167-854-1	Sequence 1, Appli
c 24	22.8	78.6	383	3	US-09-319-056B-10	Sequence 10, Appl
25	22.8	78.6	383	3	US-09-319-056B-12	Sequence 12, Appl
c 26	22.6	77.9	647	3	US-08-578-634C-1	Sequence 1, Appli
c 27	22.6	77.9	647	3	US-09-430-010-1	Sequence 1, Appli
c 28	22.6	77.9	1518	2	US-08-815-667-8	Sequence 8, Appli
c 29	22.6	77.9	1524	2	US-08-409-122-1	Sequence 1, Appli
c 30	22.6	77.9	1524	2	US-08-408-669-1	Sequence 1, Appli
c 31	22.6	77.9	1524	3	US-08-913-644-1	Sequence 1, Appli
c 32	21	72.4	386	3	US-09-319-056B-13	Sequence 13, Appl
33	21	72.4	386	3	US-09-319-056B-15	Sequence 15, Appl
c 34	21	72.4	386	3	US-09-319-056B-16	Sequence 16, Appl
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c 36	21	72.4	1518	2	US-08-815-667-9	Sequence 9, Appli
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c 40	19.6	67.6	398	3	US-09-628-099-28	Sequence 28, Appl
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c 42	19.6	67.6	398	3	US-10-056-360-28	Sequence 28, Appl
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ALIGNMENTS

RESULT 1
US-09-210-168-2/c
; Sequence 2, Application US/09210168
; Patent No. 6355424
; GENERAL INFORMATION:
; APPLICANT: Lorincz, Attila T.
; TITLE OF INVENTION: ASSESSMENT OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE
; FILE REFERENCE: 26294005US2
; CURRENT APPLICATION NUMBER: US/09/210,168
; CURRENT FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: U.S. 60/082,167
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: U.S. 60/070,486
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: U.S. 60/069,426
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Human papillomavirus
; FEATURE:
; OTHER INFORMATION: L1-HPV16
US-09-210-168-2

Query Match 83.4%; Score 24.2; DB 3; Length 1484;
Best Local Similarity 89.7%; Pred. No. 0.076;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 5, Application US/09413611A
; Patent No. 6380364
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Kast, Wijbe
; APPLICANT: Nieland, John
; APPLICANT: Velders, Markwin
; TITLE OF INVENTION: Chimeric Biotin-Binding Papillomavirus Protein
; FILE REFERENCE: 202325
; CURRENT APPLICATION NUMBER: US/09/413,611A

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;  CURRENT FILING DATE:  1999-10-06
;  PRIOR APPLICATION NUMBER:  US 60/109,510
;  PRIOR FILING DATE:  1998-11-23
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 5
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:biotin-binding
;   OTHER INFORMATION: papillomavirus protein 168
;   NAME/KEY: CDS
;   LOCATION: (1)..(1491)
US-09-413-611A-5

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; Sequence 7, Application US/09413611A
; Patent No. 6380364
; GENERAL INFORMATION:
;  APPLICANT:  Mueller, Martin
;  APPLICANT:  Kast, Wijbe
;  APPLICANT:  Nieland, John
;  APPLICANT:  Velders, Markwin
;  TITLE OF INVENTION:  Chimeric Biotin-Binding Papillomavirus Protein
;  FILE REFERENCE:  202325
;  CURRENT APPLICATION NUMBER: US/09/413,611A
;  CURRENT FILING DATE:  1999-10-06
;  PRIOR APPLICATION NUMBER:  US 60/109,510
;  PRIOR FILING DATE:  1998-11-23
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;   LOCATION: (1)..(1497)
US-09-413-611A-7

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RESULT 4
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; Sequence 1, Application US/08032869A
; Patent No. 5437951
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/032,869A
;      FILING DATE:  16-MAR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      ORGANISM:  Human papillomavirus
;      STRAIN:  HPV16
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;      NAME/KEY:  CDS
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US-08-032-869A-1

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  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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; Patent No. 5437951
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       APPLICATION NUMBER:  US/08/032,869A
;       FILING DATE:  16-MAR-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/941,371
;       FILING DATE:  03-SEP-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kirkpatrick Ph.D., Anita M.
;       REGISTRATION NUMBER:  32,617
;       REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-235-8550
;       TELEFAX:  619-235-0176
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1517 base pairs
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1517
US-08-032-869A-2

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 6
US-08-472-673-1/c
; Sequence 1, Application US/08472673
; Patent No. 5709996
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,673
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/032,869
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Human papillomavirus
;      STRAIN:  HPV16
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-472-673-1

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
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  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 7
US-08-472-673-2/c
; Sequence 2, Application US/08472673
; Patent No. 5709996
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,673
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/032,869
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-472-673-2

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 8
US-08-475-782-1/c
; Sequence 1, Application US/08475782
; Patent No. 5744142
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,782
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/032,869
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Human papillomavirus
;      STRAIN:  HPV16
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-475-782-1

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 9
US-08-475-782-2/c
; Sequence 2, Application US/08475782
; Patent No. 5744142
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/475,782
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/032,869
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-475-782-2

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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RESULT 10
US-08-472-678-1/c
; Sequence 1, Application US/08472678
; Patent No. 5871998
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,678
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/032,869A
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Human papillomavirus
;      STRAIN:  HPV16
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-472-678-1

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 11
US-08-472-678-2/c
; Sequence 2, Application US/08472678
; Patent No. 5871998
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,678
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/032,869A
;      FILING DATE:  16-MAR-1993
;      APPLICATION NUMBER:  US 07/941,371
;      FILING DATE:  03-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-472-678-2

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 12
US-08-484-503-1/c
; Sequence 1, Application US/08484503
; Patent No. 5985610
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,503
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/032,869
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Human papillomavirus
;      STRAIN:  HPV16
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-484-503-1

  Query Match             83.4%;  Score 24.2;  DB 2;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 13
US-08-484-503-2/c
; Sequence 2, Application US/08484503
; Patent No. 5985610
;  GENERAL INFORMATION:
;    APPLICANT:  Lowy, Douglas R.
;    APPLICANT:  Schiller, John T.
;    APPLICANT:  Kirnbauer, Reinhard
;    TITLE OF INVENTION:  SELF- ASSEMBLING RECOMBINANT
;    TITLE OF INVENTION:  PAPILLOMAVIRUS CAPSID PROTEINS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON & BEAR
;      STREET:  620 Newport Center Drive, Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,503
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/032,869
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kirkpatrick Ph.D., Anita M.
;      REGISTRATION NUMBER:  32,617
;      REFERENCE/DOCKET NUMBER:  NIH032.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-235-8550
;      TELEFAX:  619-235-0176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      NAME/KEY:  CDS
;      LOCATION:  1..1517
US-08-484-503-2

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  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 14
US-08-944-368A-1/c
; Sequence 1, Application US/08944368A
; Patent No. 6228368
;  GENERAL INFORMATION:
;    APPLICANT:  Gissman, et al.
;    TITLE OF INVENTION:  Papilloma Virus Capsomere Vaccine
;    TITLE OF INVENTION:  Formulations and Methods of Use
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  233 South Wacker Drive, 6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/944,368A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams Jr., Joseph A.
;      REGISTRATION NUMBER:  38,659
;      REFERENCE/DOCKET NUMBER:  27013/34028
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1518 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
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;      NAME/KEY:  CDS
;      LOCATION:  1..1518
US-08-944-368A-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.076;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 15
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; Sequence 1, Application US/09820764
; Patent No. 6352696
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/820,764
;             FILING DATE: 30-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/026,896
;             FILING DATE: 20-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
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US-09-820-764-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
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  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


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GenCore version 5.1.7

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Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	24.2	83.4	1452	9	US-10-487-719-4	Sequence 4, Appli
c	4	24.2	83.4	1484	3	US-09-970-477-2	Sequence 2, Appli
c	5	24.2	83.4	1517	3	US-09-832-065-1	Sequence 1, Appli
c	6	24.2	83.4	1517	3	US-09-832-065-2	Sequence 2, Appli
c	7	24.2	83.4	1517	6	US-10-371-846-1	Sequence 1, Appli
c	8	24.2	83.4	1517	6	US-10-371-846-2	Sequence 2, Appli
c	9	24.2	83.4	1518	3	US-09-820-765-1	Sequence 1, Appli
c	10	24.2	83.4	1518	3	US-09-162-904A-1	Sequence 1, Appli
c	11	24.2	83.4	1518	3	US-09-162-904A-2	Sequence 2, Appli
c	12	24.2	83.4	1518	3	US-09-824-017-1	Sequence 1, Appli
c	13	24.2	83.4	1518	3	US-09-986-118A-1	Sequence 1, Appli
c	14	24.2	83.4	1518	6	US-10-367-095-11	Sequence 11, Appl
c	15	24.2	83.4	1518	6	US-10-367-095-12	Sequence 12, Appl
c	16	24.2	83.4	1518	7	US-10-368-046-11	Sequence 11, Appl
c	17	24.2	83.4	1518	7	US-10-368-046-12	Sequence 12, Appl
c	18	24.2	83.4	1518	7	US-10-654-129-1	Sequence 1, Appli
c	19	24.2	83.4	1518	7	US-10-367-367-11	Sequence 11, Appl
c	20	24.2	83.4	1518	7	US-10-367-367-12	Sequence 12, Appl
c	21	24.2	83.4	1518	8	US-10-042-526A-1	Sequence 1, Appli
c	22	24.2	83.4	1518	9	US-10-487-719-1	Sequence 1, Appli
c	23	24.2	83.4	1518	9	US-10-487-719-3	Sequence 3, Appli
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c	26	24.2	83.4	1596	9	US-10-367-057-115	Sequence 115, App
c	27	24.2	83.4	7904	9	US-10-494-800-2	Sequence 2, Appli
c	28	22.6	77.9	1421	7	US-10-433-091-1	Sequence 1, Appli
c	29	22.6	77.9	8026	9	US-10-978-239-14	Sequence 14, Appl
	30	20.8	71.7	24	8	US-10-720-424B-9	Sequence 9, Appli
c	31	20.6	71.0	101209	5	US-10-087-192-460	Sequence 460, App
	32	20.2	69.7	421	4	US-09-925-065A-151425	Sequence 151425,
c	33	20	69.0	1527	9	US-10-367-057-127	Sequence 127, App
	34	19.8	68.3	33	8	US-10-720-424B-12	Sequence 12, Appl
c	35	19.6	67.6	398	5	US-10-056-359-28	Sequence 28, Appl
	36	19.6	67.6	398	5	US-10-056-359-30	Sequence 30, Appl
c	37	19.6	67.6	398	5	US-10-056-360-28	Sequence 28, Appl
	38	19.6	67.6	398	5	US-10-056-360-30	Sequence 30, Appl
c	39	19.4	66.9	575	9	US-10-779-543-17310	Sequence 17310, A
c	40	19.4	66.9	1404	8	US-10-475-203A-7	Sequence 7, Appli
c	41	19.4	66.9	1503	8	US-10-475-203A-3	Sequence 3, Appli
c	42	19	65.5	400660	8	US-10-388-838-68	Sequence 68, Appl
	43	18.8	64.8	567	4	US-09-925-065A-661735	Sequence 661735,
	44	18.8	64.8	567	4	US-09-925-065A-661736	Sequence 661736,
	45	18.6	64.1	197526	7	US-10-322-281-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-10-720-424B-8
; Sequence 8, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-8

Query Match 100.0%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              |||||||||||||||||||||||||||||
Db          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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RESULT 2
US-10-487-719-2/c
; Sequence 2, Application US/10487719
; Publication No. US20050090435A1
; GENERAL INFORMATION:
; APPLICANT: Varsani, Arvind
; APPLICANT: Tybicki, Edward
; APPLICANT: Williamson, Anna-Lise

```
;  TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
;  TITLE OF INVENTION:  Isolating Said Pharmaceutical Compositions, and Use of Said
;  TITLE OF INVENTION:  Pharmaceutical Compositions for Prophylactic Treatment of
;  TITLE OF INVENTION:  Lesions and Carcinomas
;  FILE REFERENCE: 025455-116
;  CURRENT APPLICATION NUMBER: US/10/487,719
;  CURRENT FILING DATE:  2004-02-27
;  PRIOR APPLICATION NUMBER: PCT/IB02/03531
;  PRIOR FILING DATE: 2002-08-30
;  PRIOR APPLICATION NUMBER: ZA 2001/7228
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fragment of L1 gene
US-10-487-719-2

  Query Match             83.4%;  Score 24.2;  DB 9;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 3
US-10-487-719-4/c
; Sequence 4, Application US/10487719
; Publication No. US20050090435A1
; GENERAL INFORMATION:
;  APPLICANT: Varsani, Arvind
;  APPLICANT:  Tybicki, Edward
;  APPLICANT:  Williamson, Anna-Lise
;  TITLE OF INVENTION: Pharmaceutical Compositions, and a Method of Preparing and
;  TITLE OF INVENTION:  Isolating Said Pharmaceutical Compositions, and Use of Said
;  TITLE OF INVENTION:  Pharmaceutical Compositions for Prophylactic Treatment of
;  TITLE OF INVENTION:  Lesions and Carcinomas
;  FILE REFERENCE: 025455-116
;  CURRENT APPLICATION NUMBER: US/10/487,719
;  CURRENT FILING DATE:  2004-02-27
;  PRIOR APPLICATION NUMBER: PCT/IB02/03531
;  PRIOR FILING DATE: 2002-08-30
;  PRIOR APPLICATION NUMBER: ZA 2001/7228
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 1452
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fragment of L1 gene
US-10-487-719-4

  Query Match             83.4%;  Score 24.2;  DB 9;  Length 1452;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 4
US-09-970-477-2/c
; Sequence 2, Application US/09970477
; Patent No. US20020127545A1
; GENERAL INFORMATION:
;  APPLICANT: Lorincz, Attila T.
;  TITLE OF INVENTION: ASSESSMENTS OF HUMAN PAPILLOMA VIRUS-RELATED DISEASE
;  FILE REFERENCE: 2629-4005US4
;  CURRENT APPLICATION NUMBER: US/09/970,477
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: U.S. 09/210,168
;  PRIOR FILING DATE: 1998-12-11
;  PRIOR APPLICATION NUMBER: U.S. 60/082,167
;  PRIOR FILING DATE: 1998-04-17
;  PRIOR APPLICATION NUMBER: U.S. 60/070,486
;  PRIOR FILING DATE: 1998-01-05
;  PRIOR APPLICATION NUMBER: U.S. 60/069,426
;  PRIOR FILING DATE: 1997-12-12
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1484
;   TYPE: DNA
;   ORGANISM: Human papillomavirus
;   FEATURE:
;   OTHER INFORMATION: L1-HPV16
US-09-970-477-2

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1484;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        890 GCATCAGAGGTAACCATAGAACCACTAGG 862


RESULT 5
US-09-832-065-1/c
; Sequence 1, Application US/09832065
; Publication No. US20030050439A1
;   GENERAL INFORMATION:
;        APPLICANT: Lowy, Douglas R.
;                   Schiller, John T.
;                   Kirnbauer, Reinhard
;        TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                            PAPILLOMAVIRUS CAPSID PROTEINS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;             STREET: 620 Newport Center Drive, Sixteenth Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/832,065
;             FILING DATE: 09-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/316,487
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kirkpatrick Ph.D., Anita M.
;             REGISTRATION NUMBER: 32,617
;             REFERENCE/DOCKET NUMBER: NIH032.001CP1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-235-8550
;             TELEFAX: 619-235-0176
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1517 base pairs
;             TYPE: nucleic acid
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;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         ORIGINAL SOURCE:
;             ORGANISM: Human papillomavirus
;             STRAIN: HPV16
;         FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1517
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-832-065-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 6
US-09-832-065-2/c
; Sequence 2, Application US/09832065
; Publication No. US20030050439A1
;   GENERAL INFORMATION:
;         APPLICANT: Lowy, Douglas R.
;                    Schiller, John T.
;                    Kirnbauer, Reinhard
;         TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                             PAPILLOMAVIRUS CAPSID PROTEINS
;         NUMBER OF SEQUENCES: 6
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;             STREET: 620 Newport Center Drive, Sixteenth Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/832,065
;             FILING DATE: 09-Apr-2001
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/316,487
;             FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Kirkpatrick Ph.D., Anita M.
;             REGISTRATION NUMBER: 32,617
;             REFERENCE/DOCKET NUMBER: NIH032.001CP1
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-235-8550
;             TELEFAX: 619-235-0176
;    INFORMATION FOR SEQ ID NO: 2:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 1517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1517
;         SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-832-065-2

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 7
US-10-371-846-1/c
; Sequence 1, Application US/10371846
; Publication No. US20030219873A1
;   GENERAL INFORMATION:
;         APPLICANT: Lowy, Douglas R.
;                    Schiller, John T.
;                    Kirnbauer, Reinhard
;         TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                             PAPILLOMAVIRUS CAPSID PROTEINS
;         NUMBER OF SEQUENCES: 6
;         CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;             STREET: 620 Newport Center Drive, Sixteenth Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;         COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/371,846
;             FILING DATE: 21-Feb-2003
;             CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/032,869
;             FILING DATE: 16-MAR-1993
;             APPLICATION NUMBER: US 07/941,371
;             FILING DATE: 03-SEP-1992
;         ATTORNEY/AGENT INFORMATION:
;             NAME: Kirkpatrick Ph.D., Anita M.
;             REGISTRATION NUMBER: 32,617
;             REFERENCE/DOCKET NUMBER: NIH032.001CP1
;         TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-235-8550
;             TELEFAX: 619-235-0176
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;             LENGTH: 1517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;         MOLECULE TYPE: DNA (genomic)
;         HYPOTHETICAL: NO
;         ANTI-SENSE: NO
;         ORIGINAL SOURCE:
;             ORGANISM: Human papillomavirus
;             STRAIN: HPV16
;         FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1517
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-371-846-1

  Query Match             83.4%;  Score 24.2;  DB 6;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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                    || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 8
US-10-371-846-2/c
; Sequence 2, Application US/10371846
; Publication No. US20030219873A1
;   GENERAL INFORMATION:
;        APPLICANT: Lowy, Douglas R.
;                   Schiller, John T.
;                   Kirnbauer, Reinhard
;        TITLE OF INVENTION: SELF- ASSEMBLING RECOMBINANT
;                            PAPILLOMAVIRUS CAPSID PROTEINS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: KNOBBE, MARTENS, OLSON & BEAR
;             STREET: 620 Newport Center Drive, Sixteenth Floor
;             CITY: Newport Beach
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92660
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/371,846
;             FILING DATE: 21-Feb-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/032,869
;             FILING DATE: 16-MAR-1993
;             APPLICATION NUMBER: US 07/941,371
;             FILING DATE: 03-SEP-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kirkpatrick Ph.D., Anita M.
;             REGISTRATION NUMBER: 32,617
;             REFERENCE/DOCKET NUMBER: NIH032.001CP1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619-235-8550
;             TELEFAX: 619-235-0176
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1517 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1517
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-371-846-2

  Query Match             83.4%;  Score 24.2;  DB 6;  Length 1517;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 9
US-09-820-765-1/c
; Sequence 1, Application US/09820765
; Publication No. US20020039584A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/820,765
;             FILING DATE: 30-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/026,896
;             FILING DATE: 20-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-820-765-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
                || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 10
US-09-162-904A-1/c
; Sequence 1, Application US/09162904A
; Patent No. US20020168372A1
; GENERAL INFORMATION:
;  APPLICANT: Durst, Matthias
;  APPLICANT:  Gissmann, Lutz
;  TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
;  TITLE OF INVENTION:  OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
;  FILE REFERENCE: 8484-068-999
;  CURRENT APPLICATION NUMBER: US/09/162,904A
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 08/884,168
;  PRIOR FILING DATE: 1997-06-27
;  PRIOR APPLICATION NUMBER: 08/641,570
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/902,528
;  PRIOR FILING DATE: 1993-07-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gen
;   OTHER INFORMATION: HPV16 DNA clone P114/16/2
US-09-162-904A-1

  Query Match            83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity  89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 11
US-09-162-904A-2/c
; Sequence 2, Application US/09162904A
; Patent No. US20020168372A1
; GENERAL INFORMATION:
;  APPLICANT: Durst, Matthias
;  APPLICANT:  Gissmann, Lutz
;  TITLE OF INVENTION: A DNA SEQUENCE ENCODING A PAPILLOMAVIRUS L1 PROTEIN CAPABLE
;  TITLE OF INVENTION:  OF EFFICIENTLY FORMING VIRUS-LIKE PARTICLES
;  FILE REFERENCE: 8484-068-999
;  CURRENT APPLICATION NUMBER: US/09/162,904A
;  CURRENT FILING DATE:  1998-09-29
;  PRIOR APPLICATION NUMBER: 08/884,168
;  PRIOR FILING DATE: 1997-06-27
;  PRIOR APPLICATION NUMBER: 08/641,570
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/902,528
;  PRIOR FILING DATE: 1993-07-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of L1 gen
;   OTHER INFORMATION: HPV16 DNA clone P114/16/11
US-09-162-904A-2

  Query Match            83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity  89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 12
US-09-824-017-1/c
; Sequence 1, Application US/09824017
; Publication No. US20020197668A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/824,017
;             FILING DATE: 03-Apr-2001
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/026,896
;             FILING DATE: 1998-02-20
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-824-017-1

  Query Match            83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity  89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 13
US-09-986-118A-1/c
; Sequence 1, Application US/09986118A
; Publication No. US20030021806A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/986,118A
;             FILING DATE: 07-No. US20030021806A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/026,896
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
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;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;    INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1518 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1515
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-986-118A-1

  Query Match             83.4%;  Score 24.2;  DB 3;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches   3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 14
US-10-367-095-11/c
; Sequence 11, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
;  APPLICANT: Robin A. Robinson
;  TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line
;  FILE REFERENCE: 44149-1US1
;  CURRENT APPLICATION NUMBER: US/10/367,095
;  CURRENT FILING DATE:  2003-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,119
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,161
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,118
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,133
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,157
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,156
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,123
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,113
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,154
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,135
;  PRIOR FILING DATE: 2002-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HPV-16 L1 wild type NVAX clone
US-10-367-095-11

  Query Match             83.4%;  Score 24.2;  DB 6;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches   3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 15
US-10-367-095-12/c
; Sequence 12, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
;  APPLICANT: Robin A. Robinson
;  TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line
;  FILE REFERENCE: 44149-1US1
;  CURRENT APPLICATION NUMBER: US/10/367,095
;  CURRENT FILING DATE:  2003-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,119
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,161
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,118
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,133
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,157
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,156
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,123
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,113
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,154
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US 60/356,135
;  PRIOR FILING DATE: 2002-02-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HPV-16 L1 wild type clone (GenBank K02718)
US-10-367-095-12

  Query Match             83.4%;  Score 24.2;  DB 6;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.25;
  Matches   26;  Conservative    0;  Mismatches   3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


Search completed: March  5, 2006, 22:49:28
Job time : 362 secs
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:06:14 ; Search time 457 Seconds
(without alignments)
139.129 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	24.2	83.4	1518	7	US-10-514-878A-2	Sequence 2, Appli
c	2	24.2	83.4	1518	7	US-10-514-878A-4	Sequence 4, Appli
c	3	24.2	83.4	1518	7	US-10-514-878A-6	Sequence 6, Appli
c	4	24.2	83.4	1518	7	US-10-514-878A-8	Sequence 8, Appli
c	5	24.2	83.4	1518	7	US-10-514-878A-10	Sequence 10, Appl
c	6	24.2	83.4	1518	7	US-10-514-878A-12	Sequence 12, Appl
c	7	24.2	83.4	1518	12	US-11-179-478-1	Sequence 1, Appli
	8	20.2	69.7	421	6	US-09-925-065A-151425	Sequence 151425,
	9	18.8	64.8	567	6	US-09-925-065A-661735	Sequence 661735,
	10	18.8	64.8	567	6	US-09-925-065A-661736	Sequence 661736,
	11	18	62.1	541	6	US-09-925-065A-13399	Sequence 13399, A
	12	18	62.1	541	6	US-09-925-065A-13400	Sequence 13400, A
	13	18	62.1	586	6	US-09-925-065A-537693	Sequence 537693,
c	14	18	62.1	645	6	US-09-925-065A-727186	Sequence 727186,
	15	18	62.1	1021	8	US-10-750-185-31766	Sequence 31766, A
	16	18	62.1	1021	8	US-10-750-623-31766	Sequence 31766, A
	17	18	62.1	2457	12	US-11-128-061-800	Sequence 800, App
	18	18	62.1	2457	12	US-11-128-049-800	Sequence 800, App
	19	17.8	61.4	201	8	US-10-995-561-27379	Sequence 27379, A
c	20	17.8	61.4	201	8	US-10-995-561-42693	Sequence 42693, A
c	21	17.8	61.4	201	12	US-11-124-367A-14923	Sequence 14923, A
c	22	17.8	61.4	201	12	US-11-124-367A-33222	Sequence 33222, A
	23	17.8	61.4	563	6	US-09-925-065A-689088	Sequence 689088,
	24	17.8	61.4	563	6	US-09-925-065A-689089	Sequence 689089,
	25	17.8	61.4	53641	8	US-10-995-561-13238	Sequence 13238, A
c	26	17.8	61.4	1125000	8	US-10-995-561-13286	Sequence 13286, A
	27	17.6	60.7	814	6	US-09-925-065A-54678	Sequence 54678, A
c	28	17.6	60.7	1753	8	US-10-750-185-35843	Sequence 35843, A
c	29	17.6	60.7	1753	8	US-10-750-623-35843	Sequence 35843, A
c	30	17.6	60.7	2129	6	US-09-925-065A-709891	Sequence 709891,
	31	17.6	60.7	3045	8	US-10-750-185-59924	Sequence 59924, A
	32	17.6	60.7	3045	8	US-10-750-623-59924	Sequence 59924, A
	33	17.4	60.0	449	6	US-09-925-065A-796428	Sequence 796428,
	34	17.4	60.0	449	6	US-09-925-065A-851486	Sequence 851486,
	35	17.4	60.0	454	6	US-09-925-065A-796346	Sequence 796346,
	36	17.4	60.0	454	6	US-09-925-065A-851448	Sequence 851448,
c	37	17.4	60.0	522	6	US-09-925-065A-274631	Sequence 274631,
c	38	17.4	60.0	525	6	US-09-925-065A-411761	Sequence 411761,
c	39	17.4	60.0	525	6	US-09-925-065A-411762	Sequence 411762,
c	40	17.4	60.0	526	6	US-09-925-065A-391311	Sequence 391311,
c	41	17.4	60.0	535	6	US-09-925-065A-99734	Sequence 99734, A
c	42	17.4	60.0	564	6	US-09-925-065A-103917	Sequence 103917,
c	43	17.4	60.0	587	6	US-09-925-065A-301382	Sequence 301382,
c	44	17.4	60.0	599	6	US-09-925-065A-301381	Sequence 301381,
c	45	17.4	60.0	604	6	US-09-925-065A-301380	Sequence 301380,

ALIGNMENTS

RESULT 1
US-10-514-878A-2/c
; Sequence 2, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-514-878A-2

Query Match 83.4%; Score 24.2; DB 7; Length 1518;
Best Local Similarity 89.7%; Pred. No. 0.066;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883
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RESULT 2
US-10-514-878A-4/c
; Sequence 4, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
; APPLICANT: University of Cape Town
; TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
; TITLE OF INVENTION: Preparing the Particles
; FILE REFERENCE: 10/514,878
; CURRENT APPLICATION NUMBER: US/10/514,878A
; CURRENT FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1518

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;   TYPE: DNA
;   ORGANISM: Human papillomavirus
US-10-514-878A-4

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  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 3
US-10-514-878A-6/c
; Sequence 6, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
;  APPLICANT: University of Cape Town
;  TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
;  TITLE OF INVENTION:  Preparing the Particles
;  FILE REFERENCE: 10/514,878
;  CURRENT APPLICATION NUMBER: US/10/514,878A
;  CURRENT FILING DATE:  2004-11-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Human papillomavirus
US-10-514-878A-6

  Query Match             83.4%;  Score 24.2;  DB 7;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 4
US-10-514-878A-8/c
; Sequence 8, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
;  APPLICANT: University of Cape Town
;  TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
;  TITLE OF INVENTION:  Preparing the Particles
;  FILE REFERENCE: 10/514,878
;  CURRENT APPLICATION NUMBER: US/10/514,878A
;  CURRENT FILING DATE:  2004-11-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Human papillomavirus
US-10-514-878A-8

  Query Match             83.4%;  Score 24.2;  DB 7;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 5
US-10-514-878A-10/c
; Sequence 10, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
;  APPLICANT: University of Cape Town
;  TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
;  TITLE OF INVENTION:  Preparing the Particles
;  FILE REFERENCE: 10/514,878
;  CURRENT APPLICATION NUMBER: US/10/514,878A
;  CURRENT FILING DATE:  2004-11-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
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;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Human papillomavirus
US-10-514-878A-10

  Query Match             83.4%;  Score 24.2;  DB 7;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 6
US-10-514-878A-12/c
; Sequence 12, Application US/10514878A
; Publication No. US20060035319A1
; GENERAL INFORMATION:
;  APPLICANT: University of Cape Town
;  TITLE OF INVENTION: Chimaeric Human Papillomavirus 16 L1 Virus-Like Particles and Met
;  TITLE OF INVENTION:  Preparing the Particles
;  FILE REFERENCE: 10/514,878
;  CURRENT APPLICATION NUMBER: US/10/514,878A
;  CURRENT FILING DATE:  2004-11-16
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 1518
;   TYPE: DNA
;   ORGANISM: Human papillomavirus
US-10-514-878A-12

  Query Match             83.4%;  Score 24.2;  DB 7;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 7
US-11-179-478-1/c
; Sequence 1, Application US/11179478
; Publication No. US20050249745A1
;  GENERAL INFORMATION:
;    APPLICANT:  BURGER, Alexander
;    APPLICANT:  HALLEK, Michael
;    TITLE OF INVENTION:  PAPILLOMA VIRUS CAPSOMERE VACCINE
;    TITLE OF INVENTION:  FORMULATIONS AND METHODS OF USE
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY & LARDNER
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      FILING DATE:  13-JULY-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/654,129
;      FILING DATE:  04-Sep-2003
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sandercock, Colin G.
;      REGISTRATION NUMBER:  31,298
;      REFERENCE/DOCKET NUMBER:  37067/102
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 672-5300
;      TELEFAX:  (202) 672-5399
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1518 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;     .LOCATION:  1..1515
US-11-179-478-1

  Query Match             83.4%;  Score 24.2;  DB 12;  Length 1518;
  Best Local Similarity   89.7%;  Pred. No. 0.066;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 8
US-09-925-065A-151425
; Sequence 151425, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151425
;   LENGTH: 421
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-151425

  Query Match             69.7%;  Score 20.2;  DB 6;  Length 421;
  Best Local Similarity   81.5%;  Pred. No. 4.6;
  Matches   22;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACCATAGAGCCACTAGG 29
              | |||||||| |||||:||| || |||
Db        369 GGCAGAGGTTGCCATAKAGCGACCAGG 395


RESULT 9
US-09-925-065A-661735
; Sequence 661735, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 661735
;   LENGTH: 567
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-661735

  Query Match             64.8%;  Score 18.8;  DB 6;  Length 567;
  Best Local Similarity   90.9%;  Pred. No. 23;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTACCATAGAGCCA 24
              ||||||||| ||||| ||||||
Db        383 GTCAGAGGTGACCATGGAGCCA 404


RESULT 10
US-09-925-065A-661736
; Sequence 661736, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 661736
;   LENGTH: 567
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-661736

  Query Match             64.8%;  Score 18.8;  DB 6;  Length 567;
  Best Local Similarity   90.9%;  Pred. No. 23;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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```
Qy          3 GTCAGAGGTTACCATAGAGCCA 24
              ||||||||| ||||| ||||||
Db        383 GTCAGAGGTGACCATGGAGCCA 404
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RESULT 11
US-09-925-065A-13399
; Sequence 13399, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13399
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-13399

Query Match 62.1%; Score 18; DB 6; Length 541;
Best Local Similarity 80.8%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          4 TCAGAGGTTACCATAGAGCCACTAGG 29
              ||||||| | |  ||||| |||||||
Db        262 TCAGAGGATGCAGTAGAGACACTAGG 287
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RESULT 12
US-09-925-065A-13400
; Sequence 13400, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13400
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-13400

Query Match 62.1%; Score 18; DB 6; Length 541;
Best Local Similarity 80.8%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          4 TCAGAGGTTACCATAGAGCCACTAGG 29
              ||||||| | |  ||||| |||||||
Db        262 TCAGAGGATGCAGTAGAGACACTAGG 287
```

RESULT 13
US-09-925-065A-537693
; Sequence 537693, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 537693
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-537693

Query Match 62.1%; Score 18; DB 6; Length 586;
Best Local Similarity 80.8%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 CGTCAGAGGTTACCATAGAGCCACTA 27
              | ||||||| ||||  |||| |||||
Db          8 CCTCAGAGGATACCTCAGAGTCACTA 33
```

RESULT 14
US-09-925-065A-727186/c
; Sequence 727186, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 727186
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-727186

Query Match 62.1%; Score 18; DB 6; Length 645;
Best Local Similarity 80.8%; Pred. No. 59;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              || |||||| ||||  |||||||||
Db        350 GCTTCAGAGCTTACRCCAGAGCCACT 325
```

RESULT 15
US-10-750-185-31766
; Sequence 31766, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 31766
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Bovine 19866881678791
US-10-750-185-31766

Query Match 62.1%; Score 18; DB 8; Length 1021;
Best Local Similarity 80.8%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GCGTCAGAGGTTACCATAGAGCCACT 26
              ||  ||||||||| |||||  |||||
Db        166 GCCCCAGAGGTTAACATAGGTCCACT 191
```

Search completed: March 5, 2006, 22:37:01
Job time : 458 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 21:52:50 ; Search time 907 Seconds
(without alignments)
1817.486 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	25.8	89.0	803	13	DQ003071	DQ003071 Human pap
c 2	25.8	89.0	7851	13	PPH35CG	M74117 Human papil
c 3	25.8	89.0	7852	13	HPV30	X74474 Human papil
c 4	25.8	89.0	7879	13	HPV35H	X74477 Human papil
c 5	24.4	84.1	7759	13	HPU37488	U37488 Human papil
c 6	24.4	84.1	7904	13	AF293961	AF293961 Human pap
c 7	24.2	83.4	624	13	AY098925	AY098925 Human pap
c 8	24.2	83.4	635	13	AY098921	AY098921 Human pap
c 9	24.2	83.4	667	13	AY098926	AY098926 Human pap
c 10	24.2	83.4	799	13	DQ003067	DQ003067 Human pap
c 11	24.2	83.4	1257	13	AF512011	AF512011 Human pap
c 12	24.2	83.4	1452	6	AX770809	AX770809 Sequence
c 13	24.2	83.4	1452	6	AX770811	AX770811 Sequence
c 14	24.2	83.4	1484	6	AR199234	AR199234 Sequence
c 15	24.2	83.4	1484	13	HPU34165	U34165 Human papil
c 16	24.2	83.4	1484	13	HPU34166	U34166 Human papil
c 17	24.2	83.4	1484	13	HPU34167	U34167 Human papil
c 18	24.2	83.4	1484	13	HPU34168	U34168 Human papil
c 19	24.2	83.4	1484	13	HPU34169	U34169 Human papil
c 20	24.2	83.4	1484	13	HPU34171	U34171 Human papil
c 21	24.2	83.4	1484	13	HPU34172	U34172 Human papil
c 22	24.2	83.4	1484	13	HPU34173	U34173 Human papil
c 23	24.2	83.4	1484	13	HPU34174	U34174 Human papil
c 24	24.2	83.4	1484	13	HPU34175	U34175 Human papil
c 25	24.2	83.4	1484	13	HPU34176	U34176 Human papil
c 26	24.2	83.4	1484	13	HPU34177	U34177 Human papil
c 27	24.2	83.4	1484	13	HPU34178	U34178 Human papil
c 28	24.2	83.4	1484	13	HPU34179	U34179 Human papil
c 29	24.2	83.4	1484	13	HPU34180	U34180 Human papil
c 30	24.2	83.4	1484	13	HPU34181	U34181 Human papil
c 31	24.2	83.4	1484	13	HPU34182	U34182 Human papil
c 32	24.2	83.4	1484	13	HPU34183	U34183 Human papil
c 33	24.2	83.4	1484	13	HPU34184	U34184 Human papil
c 34	24.2	83.4	1484	13	HPU34185	U34185 Human papil
c 35	24.2	83.4	1484	13	HPU34186	U34186 Human papil
c 36	24.2	83.4	1484	13	HPU34187	U34187 Human papil
c 37	24.2	83.4	1484	13	HPU34188	U34188 Human papil
c 38	24.2	83.4	1484	13	HPU34189	U34189 Human papil
c 39	24.2	83.4	1484	13	HPU34190	U34190 Human papil
c 40	24.2	83.4	1484	13	HPU34191	U34191 Human papil
c 41	24.2	83.4	1484	13	HPU34192	U34192 Human papil
c 42	24.2	83.4	1484	13	HPU34193	U34193 Human papil
c 43	24.2	83.4	1486	13	AF003031	AF003031 Human pap
c 44	24.2	83.4	1517	6	AR003253	AR003253 Sequence
c 45	24.2	83.4	1517	6	AR003254	AR003254 Sequence

ALIGNMENTS

RESULT 1
DQ003071/c
LOCUS DQ003071 803 bp DNA linear VRL 15-AUG-2005
DEFINITION Human papillomavirus type 35 nonfunctional L1 gene, partial sequence.
ACCESSION DQ003071
VERSION DQ003071.1 GI:66866327
KEYWORDS .
SOURCE Human papillomavirus type 35
ORGANISM Human papillomavirus type 35
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE 1 (bases 1 to 803)
AUTHORS Wu,X., Ren,J., Ran,D. and Ma,R.Z.
TITLE Detection of HPV types in cervical brush samples of clinical patients in Beijing and other Northern China cities
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 803)
AUTHORS Wu,X., Ren,J. and Ma,R.Z.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2005) Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, A5 Datun Raod, Chaoyang District, Beijing 100101, China
FEATURES Location/Qualifiers
source 1. .803
/organism="Human papillomavirus type 35"
/mol_type="genomic DNA"
/isolation_source="epithelial cells from cervix"
/sub_species="35"
/db_xref="taxon:10587"
/country="China"
misc_feature <1. .>803
/note="nonfunctional L1 due to mutation"
ORIGIN

Query Match 89.0%; Score 25.8; DB 13; Length 803;
Best Local Similarity 93.1%; Pred. No. 0.097;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
|| || ||||||||||||||||||||||||||

```
Db        799 GCATCGGAGGTTACCATAGAGCCACTAGG 771


RESULT 2
PPH35CG/c
LOCUS       PPH35CG                 7851 bp    DNA     circular VRL 10-MAY-2002
DEFINITION  Human papillomavirus type 35 complete genome.
ACCESSION   M74117
VERSION     M74117.1  GI:333050
KEYWORDS    complete genome; major capsid protein; minor capsid protein;
            regulatory protein; replication protein; transformer protein.
SOURCE      Human papillomavirus type 35
  ORGANISM  Human papillomavirus type 35
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (sites)
  AUTHORS   Lorincz,A.T., Quinn,A.P., Lancaster,W.D. and Temple,G.F.
  TITLE     A New Type of Papillomavirus Associated with Cancer of the Uterine
            Cervix
  JOURNAL   Virology 159, 187-190 (1991)
  MEDLINE   87265470
REFERENCE   2  (bases 1 to 7851)
  AUTHORS   Marich,J.E., Pontsler,A.V., Rice,S.M., McGraw,K.A. and
            Dubensky,T.W.
  TITLE     The phylogenetic relationship and complete nucleotide sequence of
            human papillomavirus type 35
  JOURNAL   Virology 186 (2), 770-776 (1992)
   PUBMED   1310198
COMMENT     Original source text: Human papillomavirus type 35 cervical
            carcinoma DNA.
FEATURES             Location/Qualifiers
     source          1. .7851
                     /organism="Human papillomavirus type 35"
                     /proviral
                     /mol_type="genomic DNA"
                     /isolation_source="cervical carcinoma"
                     /db_xref="taxon:10587"
     5'UTR           join(7092. .7851,1. .109)
                     /standard_name="LCR"
                     /function="regulatory region"
     protein_bind    17. .22
                     /bound_moiety="Sp-1"
     CAAT_signal     complement(18. .26)
     protein_bind    24. .35
                     /note="putative"
                     /bound_moiety="E2"
                     /function="gene transcription"
     protein_bind    39. .50
                     /note="putative"
                     /bound_moiety="E2"
                     /function="gene transcription"
     TATA_signal     54. .59
                     /note="putative"
     gene            110. .559
                     /gene="E6"
     CDS             110. .559
                     /gene="E6"
                     /note="putative; E6 ORF from bp 59 to 559"
                     /codon_start=1
                     /product="transforming protein"
                     /protein_id="AAA46966.1"
                     /db_xref="GI:333051"
                     /translation="MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYD
                     FACYDLCIVYREGQPYGVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIR
                     CITCQKPLCPVEKQRHLEEKKRFHNIGGRWTGRCMSCWKPTRRETEV"
     misc_feature    230. .238
                     /gene="E6"
                     /standard_name="Splice donor"
     misc_feature    405. .416
                     /gene="E6"
                     /standard_name="Splice acceptor"
     gene            562. .861
                     /gene="E7"
     CDS             562. .861
                     /gene="E7"
                     /note="putative"
                     /codon_start=1
                     /product="transforming protein"
                     /protein_id="AAA46967.1"
                     /db_xref="GI:333052"
                     /translation="MHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAG
                     QAKPDTSNYNIVTSCCKCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQRA"
     gene            868. .2760
                     /gene="E1"
     CDS             868. .2760
                     /gene="E1"
                     /note="putative"
                     /codon_start=1
                     /product="replication protein"
                     /protein_id="AAA46968.1"
                     /db_xref="GI:333053"
                     /translation="MADPAGTDEGEGTGCNGWFFVEAVVSRRTGSSVEDENEDDCDRG
                     EDMVDFINDTDILNIQAETETAQALFHAQEEQTHKEAVQVLKRKYASSPLSSVSLCVN
                     NNISPRLKAICIENKNTAAKRRLFELPDSGYGNSEVEIHEIQQVEGHDTVEQCSMGSG
                     DSITSSSDERHDETPTRDIIQILKCSNANAAMLAKFKELFGISFTELIRPFKSDKSTC
                     TDWCVAAFGIAPSVANFKHITYVYIYNVYRVHGAMVILALLRFKVEKREQQLKTIDAK
                     LLCISAASMLIQPPKLRSTPAALYWFKTAMSNISEVDGETPEWIQRQTVLQHSFNDAI
                     FDLSEMVQWAYDNDFIDDSDIAYKYAQLAETNSNACAFLKSNSQAKIVKDCATMCRHY
                     KRAEKREMTMSQWIKRRCAQVDDDGDWRDIVRFLRYQQVDFVAFLSALKNFLHGVPKK
                     NCILIYGAPNTGKSLFGMSLMHFLQGAIISYVNSKSHFWLQPLYDAKIAMLDDATSPC
                     GIYRPIFKKCTRWKSYISFRCKALSIVHIMPTFTYYININAGKDDRWPYLHSRVVVFT
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     gene            2693. .3796
                     /gene="E2"
     CDS             2693. .3796
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                     /note="putative"
                     /codon_start=1
                     /product="regulatory protein"
                     /protein_id="AAA46969.1"
                     /db_xref="GI:333054"
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                     YTTVPTRCLKKDVYTVEAQFDGDKQNTMHYTNWTHIYILEDSICTVVKGLVNYKGIYY
                     VHQGVETYYVTFREEAKKYGKKNIWEVHVGGQVIVCPESVFSSTELSTAEIATQLHAY
                     NTTETHTKACSVGTTETQKTNHKRLRGGTELPYNPTKRVRLSAVDSVDRGVYSTSDCT
                     NKDRCGSCSTTTPIVHLKGDANTLKCSRYRLGKYKALYQDASSTWRWTCTNDKKQIAI
                     VTLTYTTEYQRDKFLTTVKIPNTVTVSKGYMSI"
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                     /gene="E4"
     CDS             3273. .3563
                     /gene="E4"
                     /note="putative"
                     /codon_start=1
                     /product="unknown"
                     /protein_id="AAA46965.2"
                     /db_xref="GI:20522255"
                     /translation="MFVLNLYLAAQNYPLLKLLHSYTPTTPPRPIPKPAPWAPQKPRR
                     QITNDFEGVPSSPTTPPSECDSVPWTVLTEGSTLHLTAQTKTGVVVVVQLHL"
     gene            3793. .4038
                     /gene="E5"
     CDS             3793. .4038
                     /gene="E5"
                     /note="putative"
                     /codon_start=1
                     /product="E5"
                     /protein_id="AAA46970.1"
                     /db_xref="GI:333056"
                     /translation="MIDLTASSTVLLCFLLCFCVLLCLCLLVRSLLLSVSLYSALILL
                     VLILWVTVATPLLAFVVSCFCIYLWMINAHAQYLAVQ"
     polyA_signal    4159. .4164
                     /note="putative"
     gene            4184. .5593
                     /gene="L2"
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     CDS             4184. .5593
                     /gene="L2"
                     /note="putative; putative"
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ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 13;  Length 7851;
  Best Local Similarity   93.1%;  Pred. No. 0.086;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db       6487 GCATCGGAGGTTACCATAGAGCCACTAGG 6459


RESULT 3
HPV30/c
LOCUS       HPV30                   7852 bp    DNA     linear   VRL 18-APR-2005
DEFINITION  Human papillomavirus type 30 genomic DNA.
ACCESSION   X74474
VERSION     X74474.1  GI:396973
KEYWORDS    E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1
            gene; L2 gene; late protein.
SOURCE      Human papillomavirus type 30
  ORGANISM  Human papillomavirus type 30
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7852)
  AUTHORS   Delius,H. and Hofmann,B.
  TITLE     Primer-directed sequencing of human papillomavirus types
  JOURNAL   Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)
   PUBMED   8205838
REFERENCE   2  (bases 1 to 7852)
  AUTHORS   Delius,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-1993) H. Delius, Deutsches
            Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
            6900 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .7852
                     /organism="Human papillomavirus type 30"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10611"
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     CDS             102. .563
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                     EADSDMDIGATPPQQIQELLKSSNVQAKLCYKFKELFGIPFSELVRTFKSDSTCCHDW
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                     SSIVNVPSEQMLVQPPKIRSPAVALYFYKTAMSNISDIYGETPEWIQRQTQIQHSFQD
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                     /db_xref="InterPro:IPR001866"
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                     SFVEPPVIEVPQTGEVSGHILVSTPTSGVHSYEEIPMQTFAVHGTGTEPISSTPIPGL
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ORIGIN

  Query Match             89.0%;  Score 25.8;  DB 13;  Length 7852;
  Best Local Similarity   93.1%;  Pred. No. 0.086;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
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Db       6562 GCCTCAGAGGTTACCATAGACCCACTAGG 6534
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RESULT 4
HPV35H/c
LOCUS       HPV35H                  7879 bp    DNA     linear   VRL 18-APR-2005
DEFINITION  Human papillomavirus type 35H genomic DNA.
ACCESSION   X74477
VERSION     X74477.1  GI:396997
KEYWORDS    E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1
            gene; L2 gene; late protein.
SOURCE      Human papillomavirus type 35H
  ORGANISM  Human papillomavirus type 35H
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7879)
  AUTHORS   Delius,H. and Hofmann,B.
  TITLE     Primer-directed sequencing of human papillomavirus types
  JOURNAL   Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)
   PUBMED   8205838
REFERENCE   2  (bases 1 to 7879)
  AUTHORS   Delius,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-AUG-1993) H. Delius, Deutsches
            Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
            6900 Heidelberg, FRG
FEATURES             Location/Qualifiers
     source          1. .7879
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:31551"
                     /clone="insert in BamHI site of pBR322"
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     CDS             110. .559
                     /gene="E6"
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                     /protein_id="CAA52561.1"
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     gene            5601. .7109
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     CDS             5601. .7109
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                     CRPPIGEHWGKGTPCNANQVKAGECPPLELLNTVLQDGDMVDTGFGAMDFTTLQANKS
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ORIGIN

  Query Match          89.0%;  Score 25.8;  DB 13;  Length 7879;
  Best Local Similarity  93.1%;  Pred. No. 0.086;
  Matches   27;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || || ||||||||||||||||||||||||
Db       6505 GCATCGGAGGTTACCATAGAGCCACTAGG 6477


RESULT 5
HPU37488/c
LOCUS       HPU37488                7759 bp    DNA     linear   VRL 06-DEC-1999
DEFINITION  Human papillomavirus type 54, complete genome.
ACCESSION   U37488
VERSION     U37488.1  GI:1017782
KEYWORDS    .
SOURCE      Human papillomavirus - 54
  ORGANISM  Human papillomavirus - 54
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7759)
  AUTHORS   Delius,H.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7759)
  AUTHORS   Farmer,A.D.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-OCT-1995) Andrew Farmer, Los Alamos National
            Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
            Alamos, NM 87501 USA
COMMENT     HPV-54 was first isolated from a patient with condyloma acuminata.
FEATURES             Location/Qualifiers
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                     /product="transforming protein"
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                     /db_xref="GI:1017783"
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                     /protein_id="AAA79189.1"
                     /db_xref="GI:1017785"
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                     KAREMGYKVLQHQALPALAVSKGKGHKAIELQLALETLQKTVYSTEPWTLQDTCLERW
                     NAPPTGCLKRRGQTVDVIFDGHQDNTMQYVMWGDIYYQNCDGEGWTKVCSNIDAMGIY
                     YMDAEHKVYYVDFKKEASKYGEYGQWEVRMGSSIIFSPASVSSTEEALSISSTGTAEH
                     TRPANSTPRTDNSTKAIPCTPPPRKRARVYSTDQQPHSTSDPVGCDNDRHISDDNNKN
                     QGRHTSSGDTTPIVHFKGEPNTLKCFRQRIQKYKHLFEQASSTWHWACVPGTTKNRGI
                     VTLTYSSVEQRQQFLVTVRIPPSISMSLGVMSL"
     gene            3134. .3538
                     /gene="E4"
     CDS             3134. .3538
                     /gene="E4"
                     /note="putative; ORF E4 from bp 3134 to 3538"
                     /codon_start=1
                     /protein_id="AAA79191.1"
                     /db_xref="GI:1017787"
                     /translation="MQWVFIIWMQNTKCIMWILKRKHLSMGNMDSGRCVWAAASFFLL
                     HLYLVPKRHCQYPLLALLNTPDQPIPHHVPTTPQKQSRARRRLENELESTAQTSNHTA
                     PQTPWAVTTTGTSVTITTRTKDGTQVVVTLHL"
     gene            4215. .5627
                     /gene="L2"
     CDS             4215. .5627
                     /gene="L2"
                     /note="putative; ORF L2 from bp 4200 to 5627"
                     /codon_start=1
                     /product="minor capsid protein"
                     /protein_id="AAA79192.1"
                     /db_xref="GI:1017788"
                     /translation="MAKARAPRRKRASATQLYQTCKASGTCPSDVIPKVEGTTIADQI
                     LRWGSMGVFFGGLGIGTGSGTGGRTGYIPLGRPSTTLEPGPPVRPAGAVETVAPSDPS
                     IVSLVEESSVVDVGAPTPTIPSQGGFEIATSSDATPAILDVTSTTTPIRVSITSHDNP
                     IYTEPSLLDPPPPVQMDGRVLVSTSTLQSSTAENIPMDTFIIMQDHIGTTTSTPIPRP
                     PARPRLGLYSRALQQVPVQDPAFLQQPSSLITYDNPVYEGNPDVTLHFEQPTIHNAPD
                     PAFMDIFALHRPALTTRRGVVRYSRVGDRATLHTRSGLQLKPRVHFFQDLSPIAHVPE
                     EIELHPLISANNTSINNGLYSDIYDVYADTDFADTGGFSSSTVSHSSVQTALQTTSIP
                     SQYGNTTVPLTASSPYTPIPTSFRPSSGHTPFVPARPIFPQTPIAVNGGDFYLHPSYT
                     YVRKRRKRFPYFLADGYVAA"
     gene            5614. .7107
                     /gene="L1"
     CDS             5614. .7107
                     /gene="L1"
                     /note="putative; ORF L1 from bp 5422 to 7107"
                     /codon_start=1
                     /product="major capsid protein"
                     /protein_id="AAA79193.1"
                     /db_xref="GI:1017789"
                     /translation="MWRPSENKVYLPPTPVSKVVSTDEYVTRTSIYYHASSSRLLAVG
                     HPYFKVQKTNNKQSIPKVSGYQYRVFRVQLPDPNKFGLPDPSLYNPETQRLVWACTGV
                     EVGRGQPLGLGLSGHPLLNKLDDTENAPKYVGAGADNRENVSMDYKQTQLCILGCTPP
                     IGEHWAKGNLCTPNTLAAGDCPPLELVNSYIQDGDMVDIGFGAMDFKTLQTSKSEVPL
                     DVATSICKYPDYLKMAAEAYGDSLFFYLRREQMFVRHMLNRAGTMGEPVPNDLYIKKS
                     SGNLDSSIYAATPSGSMVTSEYQIFNKPYWLQRAQGQNNGICWGNQVFLTVVDTTRST
                     NLTLCATASTQDSFNNSDFREYIRHVEEYDLQFIFQLCTITLTADVMAYIHGMNPTIL
                     EDWNFGITPPATSSLEDTYRFVQSQAIACQKNNAPAKEKEDPYSKFNFWTVDLKERFS
                     SDLDQFPLGRKFLLQAGLRARPRLRPVKRAAPSSSKGTARKRAKTKR"
ORIGIN

  Query Match             84.1%;  Score 24.4;  DB 13;  Length 7759;
  Best Local Similarity   96.2%;  Pred. No. 0.44;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCATAGAGCCACTAGG 29
              ||||| ||||||||||||||||||||
Db       6503 TCAGATGTTACCATAGAGCCACTAGG 6478


RESULT 6
AF293961/c
LOCUS       AF293961                7904 bp    DNA     linear   VRL 02-APR-2001
DEFINITION  Human papillomavirus type 82 subtype IS39/AE2, complete genome.
ACCESSION   AF293961
VERSION     AF293961.1  GI:13507120
KEYWORDS    .
SOURCE      Human papillomavirus type 82
  ORGANISM  Human papillomavirus type 82
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 7904)
  AUTHORS   Terai,M. and Burk,R.D.
  TITLE     Cervical HPVs in Evolution; Genomic Sequence of IS39/AE2, a Subtype
            of Oncogenic HPV 82 (W13B)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 7904)
  AUTHORS   Burk,R.D. and Terai,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-AUG-2000) Microbiology & Immunology, Albert Einstein
            College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
FEATURES             Location/Qualifiers
     source          1. .7904
                     /organism="Human papillomavirus type 82"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:129724"
                     /note="oncogenic subtype
                     subtype: IS39/AE2"
     gene            1. .456
                     /gene="E6"
     CDS             1. .456
                     /gene="E6"
                     /codon_start=1
                     /product="putative transforming protein E6"
                     /protein_id="AAK28449.1"
                     /db_xref="GI:13507121"
                     /translation="MFEDIRERPRTLYELCEAYNTSMHNIQVLCVYCKKELCRADVYN
                     VAFTEIRIVYRDNMPYAVCKKCLMFYSRIREYRRYSRSVYGATLEAITNKSLYELLIR
                     CHRCQRPLGPEEKQKVVDDKKRFHEIAGRWTGQCANCRTAARQRSETQV"
     gene            464. .766
                     /gene="E7"
     CDS             464. .766
                     /gene="E7"
                     /codon_start=1
                     /product="putative transforming protein E7"
                     /protein_id="AAK28450.1"
                     /db_xref="GI:13507122"
                     /translation="MRGNVPQVKDIVLELTPQPEIDLQCYEQFDSSDEEDEVDNMRDQ
                     PARQAGQATCYRIKVQCCRCSSLLQLAVESSGDNLRIFQQLLMGDLSLVGPCCANN"
     gene            775. .2700
                     /gene="E1"
     CDS             775. .2700
                     /gene="E1"
                     /codon_start=1
                     /product="putative replication protein E1"
                     /protein_id="AAK28451.1"
                     /db_xref="GI:13507123"
                     /translation="MDSEGTDEEGAGCTGWFYVEAVVDKKTGDNISDDEDKNTNDTGS
                     DIIDFIDTNNSICSQAEQETARALFQVQETQAHKEAAQHLKRKFLGSPRSSPLGDITN
                     QTTQSNSQQQTTQANHPHGKRRLLDSYPDSGYGNTQVETVEATLQVDGQNGGSQHSMC
                     SGGGSSDRSTDIDLETNENTNVELNSVCAVLKCSNAKAMFMAKFKEVYGISYNELVRV
                     FKSDRTCCTDWVCALFGVSPMVAENLKTLIQPFCIYYHIQCLSCEWGTIVLMLARFTC
                     AKNRLTIAKCLGTLLNIPHSQMFIEPPKLRSTAVALYFYRTGISNISTTYGETPEWIT
                     RQTQLQHSFDDSTFELSQMVQWAFDHDVLDDSEIAFYYAQLADTDSNAAAFLKSNCQA
                     KYVKDCGTMTRHYKRAQRKSLTMSAWIRYRCDKVADGGNWREIAKFLRYQGINFMYFI
                     QTFKLFLKGTPKHNCIVIQGPPNTGKSQFAMSLIRFLQGCIISYVNSGSHFWLQPLED
                     AKIALLDDATYGCWTYIDQYLRNFLDGNPCSIDRKHRSLLQIVCPPLIITSNINPKED
                     ANLMYLHSRVTVFQFPNAFLFDPNGNPVYALNDVNWKNFFSTTWSRLDLEEEEDKENG
                     DPMSSFKCVPGENTRLL"
     gene            2642. .3721
                     /gene="E2"
     CDS             2642. .3721
                     /gene="E2"
                     /codon_start=1
                     /product="putative regulatory protein E2"
                     /protein_id="AAK28452.1"
                     /db_xref="GI:13507124"
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                     /translation="METLCHRLNVCQEKILDCYELDSDKLVDQINYWTLVRYECAMFY
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                     GEAPKQCFKKEGKTVTVMFDGNKDNTMDYTCWTYVYIYKEDRWVKTHGNVDHTGIYYK
                     PDVHKEYYVKFIEEAKKYGAQQWEVYMCGNVITCPEYVSSTCRDPLPSTTTVEQHSNT
                     PTTNTYTTSVGTKEAQAPQQRKRQRITEPDSSTVTPLSVDTCDHQIHCGTGSANTGGH
                     QSATKTAFIVHLKGATNCLKCLRYRFSKHRNLFKEVSSTWHWTSNTKAGIVTITFDSA
                     HQRQQFIDTVKVPPSVTVSLGIMTV"
     gene            3231. .3497
                     /gene="E4"
     CDS             3231. .3497
                     /gene="E4"
                     /codon_start=1
                     /product="putative E4 protein"
                     /protein_id="AAK28453.1"
                     /db_xref="GI:13507125"
                     /translation="MYLVPAETRYPLLQLLNSTRTPPRPIPIPPPWAPKKPRHHNNEN
                     DSELLSPTPPQSPHCPWTLVTTKYTVELEAQTLEGTKVQLKLRL"
     gene            <3788. .4036
                     /gene="E5"
     CDS             <3788. .4036
                     /gene="E5"
                     /note="start codon not identified"
                     /codon_start=1
                     /product="putative E5 protein"
                     /protein_id="AAK28454.1"
                     /db_xref="GI:13507126"
                     /translation="IATIAVFLVCLFVLCVCVCLVLCCLLPLLQSQYVFAAALLLIIC
                     FWFVVATSPLTTFAVYIICFYIPCLLLHLYTFYILQIP"
     gene            4068. .5489
                     /gene="L2"
     CDS             4068. .5489
                     /gene="L2"
                     /codon_start=1
                     /product="putative minor capsid protein L2"
                     /protein_id="AAK28455.1"
                     /db_xref="GI:13507127"
                     /translation="MVAARARRRKRASVTQLYSTCKAAGTCPADVIPKVEGTTLADKI
                     LQWSGLGIFLGGLGIGTGSGTGGRTGYIPLGGGGRPGVVDIAPARPPIIIEPVAPTEP
                     SIVNLVEDSSIINSGSTIPTFTGTDGFEITSSSTTTPAVLDITPSTGTVRVTSTNIEN
                     PLYIEPPPIEAPQSGEVSGHIFTSTPTSGTHGYEEIPMEVFASNVSTGEQPISSTPTP
                     GVRRIAAPRLYSKAFTQVKVTNPDFISRPSSFVTFDNPAFEPIDASLSFGEPTTVAPD
                     PDFLDIIKLHRPALTSRRGTVRFSRLGQKATIRTRSGKQIGARVHYYHDISNITPTEE
                     LEMQPLLSPSTNNYSYDIYADLDEAETGFIQPTHTTPMLRSSYSPLSTQLPSLSSSVS
                     SSYANVTIPFSTTYHVPIHTGPDVVLPTSPTVWPFIPHTSIDTQHAIVIQGGDYYLWP
                     YTYLLRKRRKRIPYFFADGFVAY"
     gene            5470. .6981
                     /gene="L1"
     CDS             5470. .6981
                     /gene="L1"
                     /codon_start=1
                     /product="putative major capsid protein L1"
                     /protein_id="AAK28456.1"
                     /db_xref="GI:13507128"
                     /translation="MALWRTNDSKVYLPPAPVSRIVNTEEYITRTGIYYYAGSSRLIT
                     LGHPYFALPKTSTRAEIPKVSAFQYRVFRVQLPDPNKFGLPDPNLFNPDTDRLVWGCV
                     GVEVGRGQPLGVGLSGHPLFNKYDDTENSRVANGNVQQDVRDNISVDNKQTQLCIIGC
                     APPIGEHWATGTTCKNVPVPQGDCPPLELVSTIIEDGDMIDTGFGAMDFANLQATKSD
                     VPLDIAQSVCKYPDYLKMSADTYGNSMFFHLRREQIFARHYYNRAGVVGDAIPDKAYI
                     KGTGTGRDPIGSYIYSATPSGSMVTSDSQIFNKPYWLHRAQGHNNGICWNNQLFITCV
                     DTTRSTNLTISTAATPSVAQTFTPTNFKQYIRHGEEYELQFIFQLCKITLTTEVMAYL
                     HTMDSTILEQWNFGLTLPPSASLEDAYRFVKNAATSCQRDSPPQAKQDPLAKYKFWTV
                     DLKERFSLDLDQLALGRKFLLQIGAQRKARPGLKRPAPSSSSSSSAKRKRVKK"
ORIGIN

  Query Match             84.1%;  Score 24.4;  DB 13;  Length 7904;
  Best Local Similarity   96.2%;  Pred. No. 0.44;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TCAGAGGTTACCATAGAGCCACTAGG 29
              ||||||||||||||||||||||| ||
Db       6377 TCAGAGGTTACCATAGAGCCACTTGG 6352
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RESULT 7
AY098925/c
LOCUS       AY098925                624 bp    DNA     linear   VRL 26-MAY-2002
DEFINITION  Human papillomavirus type 16 isolate Bsb-102 major capsid protein
            L1 (L1) gene, partial cds.
ACCESSION   AY098925
VERSION     AY098925.1  GI:21217424
KEYWORDS    .
SOURCE      Human papillomavirus type 16
  ORGANISM  Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 624)
  AUTHORS   Cruz,M.R., Cerqueira,D.M., Camara,G.N.L., Silva,E.O.,
            Carvalho,L.G.S. and Martins,C.R.F.
  TITLE     Human papillomavirus type 16 variants in Central Brazil
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 624)
  AUTHORS   Cruz,M.R. and Martins,C.R.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,
            Brasilia, DF 70.910-900, Brazil
FEATURES             Location/Qualifiers
     source          1. .624
                     /organism="Human papillomavirus type 16"
                     /virion
                     /mol_type="genomic DNA"
                     /isolate="Bsb-102, European"
                     /db_xref="taxon:333760"
                     /note="genotype: 16"
     gene            <1. .>624
                     /gene="L1"
     CDS             <1. .>624
                     /gene="L1"
                     /codon_start=1
                     /product="major capsid protein L1"
                     /protein_id="AAM29173.1"
                     /db_xref="GI:21217425"
                     /translation="HLFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTS
                     DAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTYKNTNF
                     KEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTY
                     RFVTQAIACQKHTPPAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGR"
ORIGIN

  Query Match             83.4%;  Score 24.2;  DB 13;  Length 624;
  Best Local Similarity   89.7%;  Pred. No. 0.64;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| |||||||
Db        137 GCATCAGAGGTAACCATAGAACCACTAGG 109


RESULT 8
AY098921/c
LOCUS       AY098921                635 bp    DNA     linear   VRL 26-MAY-2002
DEFINITION  Human papillomavirus type 16 isolate Bsb-178 major capsid protein
            L1 (L1) gene, partial cds.
ACCESSION   AY098921
VERSION     AY098921.1  GI:21217416
KEYWORDS    .
SOURCE      Human papillomavirus type 16
  ORGANISM  Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Cruz,M.R., Cerqueira,D.M., Camara,G.N.L., Silva,E.O.,
            Carvalho,L.G.S. and Martins,C.R.F.
  TITLE     Human papillomavirus type 16 variants in Central Brazil
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 635)
  AUTHORS   Cruz,M.R. and Martins,C.R.F.
  TITLE     Direct Submission
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  JOURNAL   Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,
            Brasilia, DF 70.910-900, Brazil
FEATURES             Location/Qualifiers
     source          1. .635
                     /organism="Human papillomavirus type 16"
                     /virion
                     /mol_type="genomic DNA"
                     /isolate="Bsb-178, Asian-american"
                     /db_xref="taxon:333760"
                     /note="genotype: 16"
     gene            <1. .>635
                     /gene="L1"
     CDS             <1. .>635
                     /gene="L1"
                     /codon_start=2
                     /product="major capsid protein L1"
                     /protein_id="AAM29169.1"
                     /db_xref="GI:21217417"
                     /translation="FVRHLFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPSGSM
                     VTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSEPTYKN
                     TNFKEYLRHGEEYDLQFIFQLCKITLTADVMSYIHSMNSTILEDWNFGLQPPPGGTLE
                     DTYRFVTQAIACQKHTPPAPKEDDPLKKYTFWEVNLKEKFSADLDQFPLGR"
ORIGIN

  Query Match             83.4%;  Score 24.2;  DB 13;  Length 635;
  Best Local Similarity   89.7%;  Pred. No. 0.64;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        147 GCATCAGAGGTAACCATAGAACCACTAGG 119


RESULT 9
AY098926/c
LOCUS       AY098926                 667 bp    DNA     linear   VRL 26-MAY-2002
DEFINITION  Human papillomavirus type 16 isolate Bsb-14 major capsid protein L1
            (L1) gene, partial cds.
ACCESSION   AY098926
VERSION     AY098926.1  GI:21217426
KEYWORDS    .
SOURCE      Human papillomavirus type 16
  ORGANISM  Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 667)
  AUTHORS   Cruz,M.R., Cerqueira,D.M., Camara,G.N.L., Silva,E.O.,
            Carvalho,L.G.S. and Martins,C.R.F.
  TITLE     Human papillomavirus type 16 variants in Central Brazil
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 667)
  AUTHORS   Cruz,M.R. and Martins,C.R.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-APR-2002) Cellular Biology, UnB, Campus UnB,
            Brasilia, DF 70.910-900, Brazil
FEATURES             Location/Qualifiers
     source          1. .667
                     /organism="Human papillomavirus type 16"
                     /virion
                     /mol_type="genomic DNA"
                     /isolate="Bsb-14, African-1"
                     /db_xref="taxon:333760"
                     /note="genotype: 16"
     gene            <1. .>667
                     /gene="L1"
     CDS             <1. .>667
                     /gene="L1"
                     /codon_start=3
                     /product="major capsid protein L1"
                     /protein_id="AAM29174.1"
                     /db_xref="GI:21217427"
                     /translation="EQMFVRHLFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPS
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                     YKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGG
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                     QAG"
ORIGIN

  Query Match             83.4%;  Score 24.2;  DB 13;  Length 667;
  Best Local Similarity   89.7%;  Pred. No. 0.64;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        157 GCATCAGAGGTAACCATAGAACCACTAGG 129


RESULT 10
DQ003067/c
LOCUS       DQ003067                 799 bp    DNA     linear   VRL 15-AUG-2005
DEFINITION  Human papillomavirus type 16 L1 gene, partial cds.
ACCESSION   DQ003067
VERSION     DQ003067.1  GI:66866320
KEYWORDS    .
SOURCE      Human papillomavirus type 16
  ORGANISM  Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 799)
  AUTHORS   Wu,X., Ren,J., Ran,D. and Ma,R.Z.
  TITLE     Detection of HPV types in cervical brush samples of clinical
            patients in Beijing and other Northern China cities
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 799)
  AUTHORS   Wu,X., Ren,J. and Ma,R.Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2005) Institute of Genetics and Developmental
            Biology, Chinese Academy of Sciences, A5 Datun Raod, Chaoyang
            District, Beijing 100101, China
FEATURES             Location/Qualifiers
     source          1. .799
                     /organism="Human papillomavirus type 16"
                     /mol_type="genomic DNA"
                     /isolation_source="epithelial cells from cervix"
                     /sub_species="16"
                     /db_xref="taxon:333760"
                     /country="China"
     CDS             <1. .>799
                     /codon_start=2
                     /product="L1"
                     /protein_id="AAY57806.1"
                     /db_xref="GI:66866321"
                     /translation="NAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVAVN
                     PGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVS
                     EPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKGSGSTANLASSNYFPTPSG
                     SMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTY
                     KNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWN"
ORIGIN

  Query Match             83.4%;  Score 24.2;  DB 13;  Length 799;
  Best Local Similarity   89.7%;  Pred. No. 0.63;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        501 GCATCAGAGGTAACCATAGAACCACTAGG 473


RESULT 11
AF512011/c
LOCUS       AF512011                1257 bp    DNA     linear   VRL 02-JUL-2002
DEFINITION  Human papillomavirus type 16 L1 protein (L1) gene, partial cds.
ACCESSION   AF512011
VERSION     AF512011.1  GI:21667875
KEYWORDS    .
SOURCE      Human papillomavirus type 16
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  ORGANISM  Human papillomavirus type 16
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            Alphapapillomavirus.
REFERENCE   1  (bases 1 to 1257)
  AUTHORS   Zhang,J. and Chen,R.
  TITLE     Cloning and sequence analysis of Human papillomavirus type 16 L1
            gene in China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1257)
  AUTHORS   Zhang,J. and Chen,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2002) Fourth Military Medical University,
            Institute of Gene Diagnosis, Changle West Road 17, Xian, Shaanxi
            710032, China
FEATURES             Location/Qualifiers
     source          1. .1257
                     /organism="Human papillomavirus type 16"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:333760"
                     /country="China"
     gene            1. .>1257
                     /gene="L1"
     CDS             1. .>1257
                     /gene="L1"
                     /codon_start=1
                     /product="L1 protein"
                     /protein_id="AAM74159.1"
                     /db_xref="GI:21667876"
                     /translation="MQVTFIYILVITCYENDVNVYHIFFQMSLWLPSEATVYLPPVPV
                     SKVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKNNNKILVPKVSGLQYRVFRIHL
                     PDPNKFGFSDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASVY
                     AANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTNVAVNPGDCPPLELINT
                     VIQDGDMVHTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLR
                     REQMFVRHLFNRAGAVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTSDAQIFNK
                     PYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTYKNTNFKEYLRHG
                     EEYDLQFIFQLCKITLTADVTTYIHSM"
ORIGIN

  Query Match           83.4%;  Score 24.2;  DB 13;  Length 1257;
  Best Local Similarity  89.7%;  Pred. No. 0.62;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        986 GCATCAGAGGTAACCATAGAACCACTAGG 958


RESULT 12
AX770809/c
LOCUS       AX770809               1452 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 2 from Patent WO03018623.
ACCESSION   AX770809
VERSION     AX770809.1  GI:32437978
KEYWORDS    .
SOURCE      Human papillomavirus
  ORGANISM  Human papillomavirus
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae.
REFERENCE   1
  AUTHORS   Varsani,A.D., Rybicki,E.P. and Williamson,A.L.
  TITLE     Pharmaceutical compositions, and a method of preparing and
            isolating said pharmaceutical compositions, and use of said
            pharmaceutical compositions for prophylactic treatment of lesions
            and carcinomas
  JOURNAL   Patent: WO 03018623-A 2 06-MAR-2003;
            University of Cape Town (ZA)
FEATURES             Location/Qualifiers
     source          1. .1452
                     /organism="Human papillomavirus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10566"
ORIGIN

  Query Match           83.4%;  Score 24.2;  DB 6;  Length 1452;
  Best Local Similarity  89.7%;  Pred. No. 0.61;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 13
AX770811/c
LOCUS       AX770811               1452 bp    DNA     linear   PAT 02-JUL-2003
DEFINITION  Sequence 4 from Patent WO03018623.
ACCESSION   AX770811
VERSION     AX770811.1  GI:32437980
KEYWORDS    .
SOURCE      Human papillomavirus
  ORGANISM  Human papillomavirus
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae.
REFERENCE   1
  AUTHORS   Varsani,A.D., Rybicki,E.P. and Williamson,A.L.
  TITLE     Pharmaceutical compositions, and a method of preparing and
            isolating said pharmaceutical compositions, and use of said
            pharmaceutical compositions for prophylactic treatment of lesions
            and carcinomas
  JOURNAL   Patent: WO 03018623-A 4 06-MAR-2003;
            University of Cape Town (ZA)
FEATURES             Location/Qualifiers
     source          1. .1452
                     /organism="Human papillomavirus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10566"
ORIGIN

  Query Match           83.4%;  Score 24.2;  DB 6;  Length 1452;
  Best Local Similarity  89.7%;  Pred. No. 0.61;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        911 GCATCAGAGGTAACCATAGAACCACTAGG 883


RESULT 14
AR199234/c
LOCUS       AR199234               1484 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2 from patent US 6355424.
ACCESSION   AR199234
VERSION     AR199234.1  GI:20249308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1484)
  AUTHORS   Lorincz,A.T. and Lazar,J.G.
  TITLE     Assessment of human papillomavirus-related disease
  JOURNAL   Patent: US 6355424-A 2 12-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .1484
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           83.4%;  Score 24.2;  DB 6;  Length 1484;
  Best Local Similarity  89.7%;  Pred. No. 0.61;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        890 GCATCAGAGGTAACCATAGAACCACTAGG 862
```

```
RESULT 15
HPU34165/c
LOCUS       HPU34165                1484 bp    DNA     linear   VRL 08-MAR-1996
DEFINITION  Human papillomavirus type 16, isolate NM 4094, late major capsid
            protein L1 (L1) gene, partial cds.
ACCESSION   U34165
VERSION     U34165.1  GI:1098837
KEYWORDS    .
SOURCE      Human papillomavirus
  ORGANISM  Human papillomavirus
            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
            unclassified Papillomaviridae.
REFERENCE   1  (bases 1 to 1484)
  AUTHORS   Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
            and Jenison,S.A.
  TITLE     Human papillomavirus type 16 variant lineages in United States
            populations characterized by nucleotide sequence analysis of the
            E6, L2, and L1 coding segments
  JOURNAL   J. Virol. 69 (12), 7743-7753 (1995)
   PUBMED   7494284
REFERENCE   2  (bases 1 to 1484)
  AUTHORS   Farmer,A.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-1995) Andrew D. Farmer, Los Alamos National
            Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
            Alamos, NM 87501, USA
FEATURES             Location/Qualifiers
     source          1. .1484
                     /organism="Human papillomavirus"
                     /mol_type="genomic DNA"
                     /isolate="NM 4094"
                     /db_xref="taxon:10566"
                     /note="collected by cervical swab at the University of New
                     Mexico, New Mexico, United States."
     gene            1. .1484
                     /gene="L1"
     CDS             <1. .>1484
                     /gene="L1"
                     /codon_start=1
                     /product="late major capsid protein L1"
                     /protein_id="AAA91712.1"
                     /db_xref="GI:1098838"
                     /translation="TVYLPPVPVSKVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIK
                     KPNNNKILVPKVSGLQYRVFRIYLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQ
                     PLGVGISGHPLLNKLDDTENASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHW
                     GKGSPCNNVAVTPGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTS
                     ICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGAVGENVPDDLYIKGSGSTAN
                     LASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMS
                     LCAAISTSEPTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMSYIHSMNSTILED
                     WNFGLQPPPGGTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADL
                     DQFPLGRKFLLQAGFKAKPKFTLGKRKATPTTSSTSTTAKRKKR"
ORIGIN

  Query Match             83.4%;  Score 24.2;  DB 13;  Length 1484;
  Best Local Similarity   89.7%;  Pred. No. 0.61;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCGTCAGAGGTTACCATAGAGCCACTAGG 29
              || |||||||| |||||||| ||||||||
Db        884 GCATCAGAGGTAACCATAGAACCACTAGG 856


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Job time : 908 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:08:34 ; Search time 271.5 Seconds
(without alignments)
711.882 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 5288170

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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10: geneseqn2003cs:*
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13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	29	12	ADQ27974	Adq27974 Human pap
c	2	14	48.3	25	9	ACI16395	Aci16395 Human mic
	3	14	48.3	38	2	AAQ23183	Aaq23183 HPV probe
	4	14	48.3	38	2	AAT29878	Aat29878 Human pap
	5	13	44.8	13	5	ABF76716	Abf76716 Oligonucl
c	6	13	44.8	13	5	ABF76717	Abf76717 Oligonucl
	7	13	44.8	17	6	ABK56011	Abk56011 Human CLC
	8	13	44.8	17	6	ABK57740	Abk57740 Human CLC
	9	13	44.8	17	6	ABK57423	Abk57423 Human CLC
	10	13	44.8	21	2	AAQ61872	Aaq61872 DNA captu
	11	13	44.8	21	2	AAV07712	Aav07712 HPV-18 pr
	12	13	44.8	21	12	ADO78152	Ado78152 Human CLC
c	13	13	44.8	21	13	ADU26858	Adu26858 Knock-dow
	14	13	44.8	24	12	ADQ27975	Adq27975 Human pap
	15	13	44.8	41	6	ABN84687	Abn84687 HIV-1 amp
	16	13	44.8	41	6	ABZ46492	Abz46492 Human ALD
	17	13	44.8	41	6	ABZ49020	Abz49020 Human ALD
	18	13	44.8	42	12	ADG00344	Adg00344 Nicotiana
	19	13	44.8	46	10	ADH94574	Adh94574 Gene prom
	20	13	44.8	61	2	AAT29759	Aat29759 D10 scTCR
	21	12	41.4	17	6	ABK57201	Abk57201 Human CLC
	22	12	41.4	17	6	ABK56012	Abk56012 Human CLC
	23	12	41.4	18	2	AAQ39483	Aaq39483 PCR Prime
	24	12	41.4	18	6	ABK40943	Abk40943 Human obe
	25	12	41.4	18	13	ADS90978	Ads90978 Oligonucl
	26	12	41.4	18	14	AEA80760	Aea80760 Human tum
	27	12	41.4	20	2	AAX94223	Aax94223 PCR prime
	28	12	41.4	20	4	AAS42900	Aas42900 Human G P
c	29	12	41.4	20	12	ADP68078	Adp68078 Human jag
	30	12	41.4	20	12	ADP68043	Adp68043 Human jag
c	31	12	41.4	21	2	AAV32488	Aav32488 Human ret
c	32	12	41.4	21	3	AAZ55850	Aaz55850 Human ret
c	33	12	41.4	23	12	ADN35455	Adn35455 Human NSC
c	34	12	41.4	25	9	ACI49246	Aci49246 Human mic
	35	12	41.4	25	9	ACK15509	Ack15509 Human mic
c	36	12	41.4	25	9	ACI16394	Aci16394 Human mic
	37	12	41.4	25	9	ACK28706	Ack28706 Human mic
	38	12	41.4	29	10	ADE37863	Ade37863 CpG islan
	39	12	41.4	29	14	ADW01878	Adw01878 DNA probe
	40	12	41.4	31	6	ABK86296	Abk86296 Human TGR
c	41	12	41.4	41	6	ABZ43753	Abz43753 Human alc
c	42	12	41.4	41	6	ABZ49321	Abz49321 Human alc
c	43	12	41.4	47	3	AAZ67316	Aaz67316 Human map
	44	12	41.4	48	4	AAS42897	Aas42897 Human G P
	45	12	41.4	50	4	AAI77901	Aai77901 Human sil

ALIGNMENTS

RESULT 1
ADQ27974
ID ADQ27974 standard; DNA; 29 BP.
XX
AC ADQ27974;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human papillomavirus genotype detection PCR primer #4.
XX
KW ss; primer; detection; diagnosis; amplification;
KW Human Papillomavirus genotype; cervical-neoplasia;
KW oncogenic high-risk group.
XX
OS Human papillomavirus.
XX
PN WO2004050917-A1.
XX
PD 17-JUN-2004.
XX
PF 28-NOV-2003; 2003WO-KR002608.
XX
PR 29-NOV-2002; 2002KR-00075370.
PR 31-JUL-2003; 2003KR-00053147.
XX
PA (ALBI-) ALBIOMED CO LTD.
XX
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;
XX
DR WPI; 2004-450746/42.
XX
PT New general primer or primer pair, useful for amplifying and detecting,
PT or for use in a nucleic acid amplification process for amplifying Human
PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT genotypes.
XX
PS Claim 1; SEQ ID NO 4; 71pp; English.
XX
CC The invention relates to a general primer or primer pair for amplifying
CC and detecting or for use in a nucleic acid amplification process for
CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC useful for amplifying cervical-neoplasia related HPV genotypes including

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CC   oncogenic high-risk groups and low-risk groups. The general primers are
CC   useful for producing amplifying products to DNA of scores of diverse
CC   oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC   sample but also to select cervical carcinoma and its pre-stage lesions at
CC   early stage by improving sensitivity according to HPV types. This
CC   sequence corresponds to PCR primer used in the invention.
XX
SQ   Sequence 29 BP; 8 A; 1 C; 11 G; 9 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 29;  DB 12;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||||||||||||||||
Db          1 GATGGTGATATGGTAGATACAGGATTTGG 29


RESULT 2
ACI16395/c
ID   ACI16395 standard; DNA; 25 BP.
XX
AC   ACI16395;
XX
DT   13-OCT-2003  (first entry)
XX
DE   Human microarray DNA oligonucleotide SEQ ID NO 16386.
XX
KW   EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW   genetic variation; biallelic marker; polymorphism; human;
KW   cross-species comparison.
XX
OS   Homo sapiens.
XX
PN   US2003104410-A1.
XX
PD   05-JUN-2003.
XX
PF   15-MAR-2002; 2002US-00098263.
XX
PR   16-MAR-2001; 2001US-0276759P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Mittmann MP;
XX
DR   WPI; 2003-567953/53.
XX
PT   New array of nucleic acid probes, useful for in situ hybridization, in
PT   Southern, Northern or dot-blot hybridization to identify or detect the
PT   sequence or specific mutations of any gene.
XX
PS   Claim 1; SEQ ID NO 16386; 9pp; English.
XX
CC   The invention discloses a microarray comprising a plurality of nucleic
CC   acid probes including one of 2,018,500 fully defined sequences, or its
CC   perfect match, perfect mismatch, antisense match or antisense mismatch.
CC   Also disclosed is a method of gene expression analysis. The array is used
CC   in monitoring gene expression levels by hybridisation to a DNA library,
CC   in analysis of genetic variation or in hybridisation of tag-labelled
CC   compounds. The nucleic acid probes are specifically designed for analysis
CC   of at least one target sequence. The method of analysis comprises
CC   hybridising at least one or more nucleic acids to at least two or more
CC   nucleic acid probes and detecting the hybridisation. The nucleic acid
CC   probes are attached to a solid support. The analysis comprises monitoring
CC   gene expression levels, identifying biallelic markers or polymorphisms,
CC   or family members of a gene and a cross-species comparison. Each of the
CC   nucleic acids further comprises a tag sequence. The array of nucleic acid
CC   probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC   blot hybridisation to identify or detect the sequence or specific
CC   mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC   primer extensions or in screening cDNA or genomic libraries or subclones
CC   for additional subclones containing segments of DNA that have been
CC   isolated and previously sequenced. The sequence presented is one of the
CC   nucleic acid probes incorporated in the microarray. Note: The sequence
CC   data for this patent can also be obtained in electronic format directly
CC   from USPTO at seqdata.uspto.goc/sequence.html
XX
SQ   Sequence 25 BP; 7 A; 7 C; 1 G; 10 T; 0 U; 0 Other;

  Query Match             48.3%;  Score 14;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 ATGGTAGATACAGG 23
               ||||||||||||||
Db          25 ATGGTAGATACAGG 12


RESULT 3
AAQ23183
ID   AAQ23183 standard; DNA; 38 BP.
XX
AC   AAQ23183;
XX
DT   06-AUG-1992  (first entry)
XX
DE   HPV probe 36.
XX
KW   Human papilloma virus; LCR; ligase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   EP477972-A.
XX
PD   01-APR-1992.
XX
PF   27-SEP-1991;   91EP-00116561.
XX
PR   28-SEP-1990;   90US-00589948.
PR   28-SEP-1990;   90US-00590105.
PR   28-SEP-1990;   90US-00590253.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Joseph JL,  Bouma SR,  Marshall RL,  Laffler TG;
XX
DR   WPI; 1992-106365/14.
XX
PT   Compsns. for amplifying DNA of human papilloma virus by LCR and PCR - and
PT   consensus and type specific oligo-nucleotide(s), for diagnosis of HPV-
PT   esp. types 6,11,16,18 33 and 61.
XX
PS   Claim 18 + Example 5; Page 69 + 11-13; 76pp; English.
XX
CC   Probe 36 maps to HPV types 6 (6365-6402), 11 (6350-6387), 16 (6225-6262),
CC   18 (6201-6238) and 33 (6182-6219). Sequences were selected according to
CC   an unique algorithm developed to choose consensus sequences. The
CC   sequences represented in AAQ23167-88 are consensus sequences selected so
CC   each should hybridise with each of human HPV types 6, 11, 16, 18 and 33.
CC   The sequences represented in AAQ23095-189 and AAQ25590 allow the
CC   detection of small amts. of HPV DNA, e.g. from cervical lesion samples,
CC   using PCR or LCR amplification procedures. The use of nucleic acids
CC   allows greater discrimination among viral subtypes than antibodies, and
CC   the use of DNA-based tests increases both the sensitivity and the
CC   specificity of prior-art antibody based tests. The oligonucleotides can
CC   be used either to detect specific sequences of specific HPV types, or
CC   consensus regions with homology among different types
XX
SQ   Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;

  Query Match             48.3%;  Score 14;  DB 2;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGT 14
```

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                  ||||||||||||||
Db          1 GATGGTGATATGGT 14


RESULT 4
AAT29878
ID   AAT29878 standard; DNA; 38 BP.
XX
AC   AAT29878;
XX
DT   25-MAR-2003  (revised)
DT   19-JUL-1996  (first entry)
XX
DE   Human papillomavirus detection probe 36.
XX
KW   primer; probe; human papillomvirus; PCR; amplification; LCR; ligation;
KW   fluorescein; biotin; ss.
XX
OS   Synthetic.
XX
PN   US5484699-A.
XX
PD   16-JAN-1996.
XX
PF   30-SEP-1994;   94US-00316293.
XX
PR   28-SEP-1990;   90US-00589948.
PR   28-SEP-1990;   90US-00590105.
PR   28-SEP-1990;   90US-00590253.
PR   22-OCT-1992;   92US-00965665.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Marshall RL,  Bouma SR,  Laffler TG,  Joseph JL;
XX
DR   WPI; 1996-087060/09.
XX
PT   New human papilloma virus type-specific oligo:nucleotide(s) - used for
PT   the detection of and determination of the type of HPV in test samples.
XX
PS   Example 5; Col 13-14; 37pp; English.
XX
CC   The sequences AAT29826-T29921 represent primers and probes derived from
CC   human papillomvirus genomic sequences and are used to detect the presence
CC   of human papillomavirus types 6, 11, 16, 18, 31 and 33 in samples. The
CC   detection is either by PCR or LCR. Alternatively the sequences can be
CC   labelled with fluorescein or biotin and used as probes. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 38 BP; 8 A; 3 C; 14 G; 13 T; 0 U; 0 Other;

  Query Match             48.3%;  Score 14;  DB 2;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGT 14
              ||||||||||||||
Db          1 GATGGTGATATGGT 14


RESULT 5
ABF76716
ID   ABF76716 standard; DNA; 13 BP.
XX
AC   ABF76716;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 176713 for detecting SNP TSC0043853.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 176713; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 5;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GGTGATATGGTAG 16
              |||||||||||||
Db          1 GGTGATATGGTAG 13


RESULT 6
ABF76717/c
ID   ABF76717 standard; DNA; 13 BP.
XX
AC   ABF76717;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 176714 for detecting SNP TSC0043853.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
```

PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 176714; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGTGATATGGTAG 16
||||||||||||
Db 13 GGTGATATGGTAG 1

RESULT 7
ABK56011
ID ABK56011 standard; RNA; 17 BP.
XX
AC ABK56011;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #382.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 59; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 6 A; 2 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.3e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ATGGTAGATACAG 22
|:||:|||:||||
Db 4 AUGGUAGAUACAG 16

RESULT 8
ABK57740
ID ABK57740 standard; RNA; 17 BP.
XX
AC ABK57740;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #2111.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 134; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down

```
CC   regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC   by cleaving RNA derived from the genes. The nucleic acid sequences are
CC   useful as pharmaceutical agents for treating conditions such as chronic
CC   obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC   fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC   that are related to or will respond to the levels of CLCA1 in a cell or
CC   tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC   hence, are useful for treatment of a patient having a condition
CC   associated with the level of CLCA1, where the invention further comprises
CC   the use of one or more therapies under conditions suitable for the
CC   treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC   antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC   nucleic acids of the invention are also used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of CLCA1 RNA in a cell. This sequence represents an
CC   enzymatic nucleic acid molecule of the invention
XX
SQ   Sequence 17 BP; 6 A; 1 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 6;  Length 17;
  Best Local Similarity   76.9%;  Pred. No. 1.3e+03;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          3 AUGGUAGAUACAG 15


RESULT 9
ABK57423
ID   ABK57423 standard; RNA; 17 BP.
XX
AC   ABK57423;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human CLCA1 gene enzymatic nucleic acid #1794.
XX
KW   Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW   antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW   chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW   oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW   acetylcysteine.
XX
OS   Homo sapiens.
XX
PN   WO200211674-A2.
XX
PD   14-FEB-2002.
XX
PF   09-AUG-2001; 2001WO-US024970.
XX
PR   09-AUG-2000; 2000US-0224383P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (SYNT ) SYNTEX USA LLC.
PA   (THOM/) THOMPSON J.
XX
PI   Thompson J,  Mcswiggen J,  Mckenzie T,  Ayers D,  Szymkowski DE;
PI   Grupe A;
XX
DR   WPI; 2002-217145/27.
XX
PT   Enzymatic polynucleotide that down regulates expression of chloride
PT   channel calcium activated gene, useful for treating Chronic obstructive
PT   pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS   Claim 4; Page 113; 152pp; English.
XX
CC   The invention relates to enzymatic nucleic acid molecules that down
CC   regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC   by cleaving RNA derived from the genes. The nucleic acid sequences are
CC   useful as pharmaceutical agents for treating conditions such as chronic
CC   obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC   fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC   that are related to or will respond to the levels of CLCA1 in a cell or
CC   tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC   hence, are useful for treatment of a patient having a condition
CC   associated with the level of CLCA1, where the invention further comprises
CC   the use of one or more therapies under conditions suitable for the
CC   treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC   antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC   nucleic acids of the invention are also used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of CLCA1 RNA in a cell. This sequence represents an
CC   enzymatic nucleic acid molecule of the invention
XX
SQ   Sequence 17 BP; 6 A; 1 C; 5 G; 0 T; 5 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 6;  Length 17;
  Best Local Similarity   76.9%;  Pred. No. 1.3e+03;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          2 AUGGUAGAUACAG 14


RESULT 10
AAQ61872
ID   AAQ61872 standard; DNA; 21 BP.
XX
AC   AAQ61872;
XX
DT   25-MAR-2003  (revised)
DT   25-OCT-1994  (first entry)
XX
DE   DNA capture probe for detection of HPV-18 by sandwich assay.
XX
KW   Human papilloma virus; HPV; detection; assay; cervical cancer;
KW   nucleic acid hybridisation; capture probe; sandwich assay; ss.
XX
OS   Synthetic.
XX
PN   WO9406933-A1.
XX
PD   31-MAR-1994.
XX
PF   21-SEP-1993;   93WO-BE000063.
XX
PR   22-SEP-1992;   92BE-00000827.
XX
PA   (LAMB-) LAMBDATECH SA.
XX
PI   Remacle J,  Rentier B,  Alexandre I,  Morris P,  Zammatteo N;
XX
DR   WPI; 1994-118481/14.
XX
PT   New conjugate for bio:luminescent hybridisation or immunoassay -
PT   comprises kinase or dehydrogenase coupled to specific ligand for the
PT   analyte, partic. for detecting human papilloma virus.
XX
PS   Example 2B; Page 23; 43pp; French.
XX
CC   The capture oligonucleotide AAQ61872 has unique specificity for the HPV-
CC   18 genome and is complementary to the region around nucleotide 6779 of
CC   HPV-18. The capture probe is immobilised for use in a sandwich
CC   hybridisation assay. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 21 BP; 5 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGG 13
```

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                  ||||||||||||
Db          9 GATGGTGATATGG 21


RESULT 11
AAV07712
ID   AAV07712 standard; DNA; 21 BP.
XX
AC   AAV07712;
XX
DT   25-NOV-1998  (first entry)
XX
DE   HPV-18 primer.
XX
KW   HPV-18; CMV; cytomegalovirus; detection; quantifying; target nucleotide;
KW   capture probe; PCR; primer; ss.
XX
OS   Synthetic.
OS   Human papillomavirus.
XX
PN   WO9811253-A2.
XX
PD   19-MAR-1998.
XX
PF   09-SEP-1997;   97WO-BE000102.
XX
PR   09-SEP-1996;   96BE-00000755.
PR   20-MAR-1997;   97BE-00000244.
XX
PA   (REMA/) REMACLE J.
XX
PI   Remacle J,  Alexandre I,  Zammatteo N,  Ernest I;
XX
DR   WPI; 1998-207411/18.
XX
PT   Sandwich-type nucleic acid hybridisation assay - using long, highly
PT   complementary capture probe.
XX
PS   Example 1; Page 43; 77pp; French.
XX
CC   The invention relates to a method for detecting and/or quantifying a
CC   target nucleotide sequence in a biological sample. It comprises
CC   contacting the sample with an immobilised capture probe and a labelled
CC   detection probe. The capture probe is a single-stranded oligonucleotide
CC   that is complementary to part of the target sequence and is covalently
CC   coupled at one end to a solid support. The detection probe is
CC   complementary to another part of the target sequence. The capture probe
CC   has a length of 50-500 bases, and a portion of the capture probe that
CC   does not hybridise with the target sequence. Use of long, highly
CC   complementary capture probes improves specificity and sensitivity. The
CC   present sequence represents a human papillomavirus (HPV)-18 primer
XX
SQ   Sequence 21 BP; 5 A; 0 C; 8 G; 8 T; 0 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGG 13
              |||||||||||||
Db          9 GATGGTGATATGG 21


RESULT 12
ADO78152
ID   ADO78152 standard; DNA; 21 BP.
XX
AC   ADO78152;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human CLCA1 RT-PCR primer #1.
XX
KW   ss; reverse transcriptase; RT-PCR; primer; tumour-associated antigen;
KW   TAg; cancer; lung cancer; breast cancer; prostate cancer; colon cancer;
KW   stomach cancer; pancreatic cancer; ear cancer; nose cancer;
KW   throat cancer; kidney cancer; cervical cancer; melanoma; tumour; human;
KW   CLCA1.
XX
OS   Homo sapiens.
XX
PN   DE10254601-A1.
XX
PD   03-JUN-2004.
XX
PF   22-NOV-2002; 2002DE-01054601.
XX
PR   22-NOV-2002; 2002DE-01054601.
XX
PA   (GANY-) GANYMED PHARM AG.
XX
PI   Tuereci O,  Sahin U,  Koslowski M;
XX
DR   WPI; 2004-421820/40.
XX
PT   Composition containing inhibitor of expression or activity of specific
PT   tumor-associated antigens, useful for treating cancers, also related
PT   compositions for diagnosis and monitoring.
XX
PS   Example 6; SEQ ID NO 67; 124pp; German.
XX
CC   The invention relates to pharmaceutical compositions that comprise an
CC   agent that inhibits the expression or activity of a tumour-associated
CC   antigen (TAg) that is encoded by a nucleic acid. The pharmaceutical
CC   compositions and related compositions, are used for treatment of diseases
CC   associated with (abnormal) expression of TAg, specifically cancer e.g. of
CC   lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney
CC   or cervix, also melanoma. Compositions containing TAg, or related nucleic
CC   acid, antibodies or host cells, are also useful for diagnosis and
CC   monitoring of tumours. The present sequence represents a human CLCA1
CC   reverse transcriptase (RT)-PCR primer.
XX
SQ   Sequence 21 BP; 8 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             44.8%;  Score 13;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
              |||||||||||||
Db          7 ATGGTAGATACAG 19


RESULT 13
ADU26858/c
ID   ADU26858 standard; DNA; 21 BP.
XX
AC   ADU26858;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Knock-down target sequence #256.
XX
KW   ds; RNA production; protein production; drug development;
KW   knock-down target.
XX
OS   Unidentified.
XX
PN   WO2004094636-A1.
XX
PD   04-NOV-2004.
XX
PF   24-APR-2003; 2003WO-EP004362.
XX
PR   24-APR-2003; 2003WO-EP004362.
XX
```

PA (GALA-) GALAPAGOS GENOMICS NV.
PA (VSCH/) VAN DER SCHUEREN J.
XX
PI Arts GJF, Lambrecht MJY, Djokic K, Clasen RJ, Mesic E;
PI Griffioen S, Bergs CJL;
XX
DR WPI; 2004-775940/76.
XX
PT New knockdown sequences, useful in lowering the amount of RNA and/or
PT protein production in cells used in drug development process.
XX
PS Claim 11; SEQ ID NO 259; 402pp; English.
XX
CC The invention relates to a polynucleotide comprising an RNA sequence. The
CC polynucleotides, vector, libraries, and method are useful in lowering the
CC amount of RNA and/or protein production in cells used in drug development
CC process. The present sequence represents a knock-down target sequence.
XX
SQ Sequence 21 BP; 5 A; 8 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTGATATGGTAGA 17
||||||||||||
Db 21 GTGATATGGTAGA 9

RESULT 14
ADQ27975
ID ADQ27975 standard; DNA; 24 BP.
XX
AC ADQ27975;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human papillomavirus genotype detection PCR primer #5.
XX
KW ss; primer; detection; diagnosis; amplification;
KW Human Papillomavirus genotype; cervical-neoplasia;
KW oncogenic high-risk group.
XX
OS Human papillomavirus.
XX
PN WO2004050917-A1.
XX
PD 17-JUN-2004.
XX
PF 28-NOV-2003; 2003WO-KR002608.
XX
PR 29-NOV-2002; 2002KR-00075370.
PR 31-JUL-2003; 2003KR-00053147.
XX
PA (ALBI-) ALBIOMED CO LTD.
XX
PI Lee S, Kim Y, Yu K, Kim S, Cha K, Ko J;
XX
DR WPI; 2004-450746/42.
XX
PT New general primer or primer pair, useful for amplifying and detecting,
PT or for use in a nucleic acid amplification process for amplifying Human
PT Papillomavirus (HPV) genotypes as well as cervical-neoplasia related HPV
PT genotypes.
XX
PS Claim 1; SEQ ID NO 5; 71pp; English.
XX
CC The invention relates to a general primer or primer pair for amplifying
CC and detecting or for use in a nucleic acid amplification process for
CC amplifying Human Papillomavirus (HPV) genotypes. The general primers are
CC useful for amplifying cervical-neoplasia related HPV genotypes including
CC oncogenic high-risk groups and low-risk groups. The general primers are
CC useful for producing amplifying products to DNA of scores of diverse
CC oncogenic HPV types and thus detecting the oncogenic HPV types in a
CC sample but also to select cervical carcinoma and its pre-stage lesions at
CC early stage by improving sensitivity according to HPV types. This
CC sequence corresponds to PCR primer used in the invention.
XX
SQ Sequence 24 BP; 6 A; 2 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 12; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ATACAGGATTTGG 29
||||||||||||
Db 12 ATACAGGATTTGG 24

RESULT 15
ABN84687
ID ABN84687 standard; DNA; 41 BP.
XX
AC ABN84687;
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
DE HIV-1 amplification primer QAL48.
XX
KW HIV-1; detection; primer; strand displacement amplification; SDA;
KW polymerase; enzyme; pol gene; ss.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT misc_binding 25. .41
FT /*tag= a
FT /bound_moiety= "HIV-1 pol gene"
FT /note= "target binding sequence"
XX
PN EP1223227-A2.
XX
PD 17-JUL-2002.
XX
PF 10-DEC-2001; 2001EP-00129200.
XX
PR 09-JAN-2001; 2001US-00757207.
XX
PA (BECT) BECTON DICKINSON & CO.
XX
PI Hellyer TJ, You Q, Harris JM;
XX
DR WPI; 2002-620683/67.
XX
PT Novel oligonucleotide useful for detecting multiple human
PT immunodeficiency virus-1 genotypes, has sequence consisting of target
PT binding sequence and optionally, a sequence for selected
PT amplification/detection reaction.
XX
PS Claim 1; Page 3; 16pp; English.
XX
CC The present sequence is that of amplification primer QAL48. This is one
CC of a set of claimed amplification and detector primers and probes (see
CC ABN84687-723) derived from the HIV-1 polymerase (pol) gene, which
CC facilitate the detection and/or quantification of all presently known
CC genotypes of HIV-1 (A-I and O). These primers and probes can be used in a
CC variety of amplification and non-amplification formats for the detection
CC of HIV nucleic acids. The present primer contains a 3' target binding
CC sequence. The remaining 5' portion of the primer comprises a restriction
CC endonuclease recognition site that is required for a strand displacement
CC amplification (SDA) reaction to proceed, and a generic non-target-
CC specific tail sequence. The 'L' in the primer name indicates a 'left'
CC primer. The target binding sequence of the primer may alternatively be
CC used as a hybridisation probe for direct detection of HIV-1, either
CC without prior amplification or as a post-amplification assay. The primers

CC and probes are useful for detecting multiple HIV-1 genotypes, and provide
CC real-time detection of HIV-1. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 41 BP; 10 A; 11 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 44.8%; Score 13; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 GGTAGATACAGGA 24
               |||||||||||||
Db          23 GGTAGATACAGGA 35
```

Search completed: March 5, 2006, 22:33:21
Job time : 275.5 secs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:12:24 ; Search time 1167.5 Seconds
(without alignments)
1411.957 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2524774

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	14	48.3	69	9	AY895594	AY895594 Mus muscu
c	2	13	44.8	31	9	MMIG23M	X82732 M.musculus
c	3	13	44.8	65	6	CQ532740	CQ532740 Sequence
c	4	13	44.8	69	9	AY895739	AY895739 Mus muscu
c	5	13	44.8	93	6	CQ144071	CQ144071 Sequence
c	6	13	44.8	93	6	CQ302512	CQ302512 Sequence
c	7	13	44.8	93	6	CQ339689	CQ339689 Sequence
	8	12	41.4	19	6	AR574640	AR574640 Sequence
	9	12	41.4	19	6	AR574641	AR574641 Sequence
	10	12	41.4	19	6	AR574642	AR574642 Sequence
	11	12	41.4	19	6	AX132750	AX132750 Sequence
	12	12	41.4	19	6	AX132751	AX132751 Sequence
	13	12	41.4	19	6	AX132752	AX132752 Sequence
	14	12	41.4	23	6	CQ855710	CQ855710 Sequence
	15	12	41.4	23	6	CQ867591	CQ867591 Sequence
	16	12	41.4	23	11	CS000569	CS000569 Sequence
c	17	12	41.4	50	6	CS026193	CS026193 Sequence
c	18	12	41.4	50	6	CS026202	CS026202 Sequence
	19	12	41.4	51	9	AY895689	AY895689 Mus muscu
c	20	12	41.4	60	6	CQ539360	CQ539360 Sequence
	21	12	41.4	65	6	CQ532263	CQ532263 Sequence
	22	12	41.4	65	6	CQ555881	CQ555881 Sequence
c	23	12	41.4	65	6	CQ557576	CQ557576 Sequence
c	24	12	41.4	68	6	CQ871437	CQ871437 Sequence
c	25	12	41.4	78	9	AY895820	AY895820 Mus muscu
c	26	12	41.4	88	2	SVI549277	AJ549277 Septifer
c	27	12	41.4	89	2	LLI549278	AJ549278 Lithophag
	28	11	37.9	11	6	CQ837879	CQ837879 Sequence
	29	11	37.9	11	6	AX629697	AX629697 Sequence
c	30	11	37.9	17	6	AX104554	AX104554 Sequence
c	31	11	37.9	17	6	AX355484	AX355484 Sequence
c	32	11	37.9	17	6	AX547607	AX547607 Sequence
	33	11	37.9	17	6	AX672986	AX672986 Sequence
	34	11	37.9	17	6	AX731253	AX731253 Sequence
	35	11	37.9	17	6	AX756776	AX756776 Sequence
	36	11	37.9	17	6	AX758708	AX758708 Sequence
	37	11	37.9	17	6	AX760520	AX760520 Sequence
	38	11	37.9	18	6	A25715	A25715 B1-8LPRB pr
	39	11	37.9	18	6	AR051387	AR051387 Sequence
c	40	11	37.9	18	6	BD096088	BD096088 Rice pero
	41	11	37.9	18	6	AX838176	AX838176 Sequence
	42	11	37.9	19	6	AR292987	AR292987 Sequence
c	43	11	37.9	20	6	AR031018	AR031018 Sequence
c	44	11	37.9	20	6	AR136805	AR136805 Sequence
c	45	11	37.9	20	6	AR139619	AR139619 Sequence

ALIGNMENTS

RESULT 1
AY895594/c
LOCUS AY895594 69 bp mRNA linear ROD 19-JUN-2005
DEFINITION Mus musculus clone RLS1415D immunoglobulin heavy chain (Igh) mRNA, partial cds.
ACCESSION AY895594
VERSION AY895594.1 GI:62634981
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 69)
AUTHORS Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,G.L., Zemlin,M. and Schroeder,H.W. Jr.
TITLE Development of the Expressed Ig CDR-H3 Repertoire Is Marked by Focusing of Constraints in Length, Amino Acid Use, and Charge That Are First Established in Early B Cell Progenitors
JOURNAL J. Immunol. 174 (12), 7773-7780 (2005)
PUBMED 15944280
REFERENCE 2 (bases 1 to 69)
AUTHORS Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,L.L., Zemlin,M. and Schroeder,H.W. Jr.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2005) Departments of Microbiology, Pediatrics and Medicine, University of Alabama at Birmingham, 1530 3rd Ave S, Birmingham, AL 35294-3300, USA
FEATURES Location/Qualifiers
source 1. .69
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/cJ"
/db_xref="taxon:10090"
/clone="RLS1415D"
/cell_type="B lymphocyte"
/tissue_type="bone marrow"
/note="CD19+,IgKappa-,IgLambda-,BP-1+,CD43-"
gene <1. .>69
/gene="Igh"
CDS <1. .>69

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                     /gene="Igh"
                     /note="complementarity determining region 3"
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAX90362.1"
                     /db_xref="GI:62634982"
                     /translation="CARLYGNYAMDYWGQGTSVTVSS"
ORIGIN

  Query Match             48.3%;  Score 14;  DB 9;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAGCC 23
               ||||||||||||||
Db         21 GTTACCATAGAGCC 8


RESULT 2
MMIG23M/c
LOCUS       MMIG23M                   31 bp    mRNA    linear   ROD 22-MAR-1995
DEFINITION  M.musculus mRNA for immunoglobulin heavy chain mu VH7183-JH4
            (ID:IG23-).
ACCESSION   X82732
VERSION     X82732.1  GI:600654
KEYWORDS    diversity region; immunoglobulin; joining region; N region;
            variable region.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Appasamy,P.M., Weng,Y., Kenniston,T.W., Albert,B.D., DeLeo,B. and
            Tang,L.
  TITLE     Expression of diverse and functional TCR V gamma 4 and V gamma 6
            transcripts with N region diversity in fetal liver cells cultured
            with interleukin 7
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 31)
  AUTHORS   Appasamy,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-NOV-1994) P.M. Appasamy, Pittsburgh Cancer Institute,
            University of Pittsburgh, DeSoto and O'Hara Streets, Pittsburgh,
            Pennsylvania PA 15213, USA
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /isolate="IG23-"
                     /db_xref="taxon:10090"
                     /cell_type="liver cells cultured without interleukin 7"
                     /tissue_type="liver"
                     /dev_stage="fetus"
     gene            1. .31
                     /gene="IgH"
     V_region        <1. .7
                     /gene="IgH"
                     /note="V region"
     N_region        8. .9
                     /gene="IgH"
                     /note="N region"
     D_segment       10. .19
                     /gene="IgH"
                     /note="D region"
     J_segment       20. .>31
                     /gene="IgH"
                     /note="J region"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 9;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAGC 22
               |||||||||||||
Db         19 GTTACCATAGAGC 7


RESULT 3
CQ532740/c
LOCUS       CQ532740                  65 bp    DNA     linear   PAT 30-JAN-2004
DEFINITION  Sequence 2375 from Patent WO0210449.
ACCESSION   CQ532740
VERSION     CQ532740.1  GI:41499004
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1
  AUTHORS   Shoshan,A., Wasserman,A., Mintz,E., Mintz,L. and Faigler,S.
  TITLE     Oligonucleotide library for detecting rna transcripts and splice
            variants that populate a transcriptome
  JOURNAL   Patent: WO 0210449-A 2375 07-FEB-2002;
            Compugen Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Rattus norvegicus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10116"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 6;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ACCATAGAGCCAC 25
               |||||||||||||
Db         34 ACCATAGAGCCAC 22


RESULT 4
AY895739/c
LOCUS       AY895739                  69 bp    mRNA    linear   ROD 19-JUN-2005
DEFINITION  Mus musculus clone III0428F immunoglobulin heavy chain (Igh) mRNA,
            partial cds.
ACCESSION   AY895739
VERSION     AY895739.1  GI:62635271
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 69)
  AUTHORS   Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,G.L., Zemlin,M.
            and Schroeder,H.W. Jr.
  TITLE     Development of the Expressed Ig CDR-H3 Repertoire Is Marked by
            Focusing of Constraints in Length, Amino Acid Use, and Charge That
            Are First Established in Early B Cell Progenitors
  JOURNAL   J. Immunol. 174 (12), 7773-7780 (2005)
   PUBMED   15944280
REFERENCE   2  (bases 1 to 69)
  AUTHORS   Ivanov,I.I., Schelonka,R.L., Zhuang,Y., Gartland,L.L., Zemlin,M.
            and Schroeder,H.W. Jr.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-2005) Departments of Microbiology, Pediatrics and
            Medicine, University of Alabama at Birmingham, 1530 3rd Ave S,
            Birmingham, AL 35294-3300, USA
FEATURES             Location/Qualifiers
     source          1. .69
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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                     /strain="BALB/cJ"
                     /db_xref="taxon:10090"
                     /clone="III0428F"
                     /cell_type="B lymphocyte"
                     /tissue_type="bone marrow"
                     /note="B220+,IgM+,IgD+"
     gene            <1. .>69
                     /gene="Igh"
     CDS             <1. .>69
                     /gene="Igh"
                     /note="complementarity determining region 3"
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAX90507.1"
                     /db_xref="GI:62635272"
                     /translation="CARVGYGNLFAYWGQGTLVTVSA"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 9;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 AGAGGTTACCATA 18
              |||||||||||||
Db         28 AGAGGTTACCATA 16


RESULT 5
CQ144071/c
LOCUS       CQ144071                  93 bp    DNA     linear   PAT 21-JAN-2004
DEFINITION  Sequence 14093 from Patent WO0157276.
ACCESSION   CQ144071
VERSION     CQ144071.1  GI:41101443
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
  TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human bone marrow
  JOURNAL   Patent: WO 0157276-A 14093 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="MAP TO AC009225.1
                     EXPRESSED IN BONE MARROW, SIGNAL = 4.1
                     NT HIT: gi4501912, EVALUE 2.00e-28
                     EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 6;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ATAGAGCCACTAG 28
              |||||||||||||
Db         58 ATAGAGCCACTAG 46


RESULT 6
CQ302512/c
LOCUS       CQ302512                  93 bp    DNA     linear   PAT 23-JAN-2004
DEFINITION  Sequence 13617 from Patent WO0186003.
ACCESSION   CQ302512
VERSION     CQ302512.1  GI:41263089
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
  TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human lung
  JOURNAL   Patent: WO 0186003-A 13617 15-NOV-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="MAP TO AC009225.1
                     EXPRESSED IN LUNG, SIGNAL = 1.1
                     NT HIT: gi4501912, EVALUE 2.00e-28
                     EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 6;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ATAGAGCCACTAG 28
              |||||||||||||
Db         58 ATAGAGCCACTAG 46


RESULT 7
CQ339689/c
LOCUS       CQ339689                  93 bp    DNA     linear   PAT 23-JAN-2004
DEFINITION  Sequence 13783 from Patent WO0157275.
ACCESSION   CQ339689
VERSION     CQ339689.1  GI:41288760
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Penn,S.G., Hanzel,D.K., Chen,W. and Rank,D.R.
  TITLE     Human genome-derived single exon nucleic acid probes useful for
            analysis of gene expression in human brain
  JOURNAL   Patent: WO 0157275-A 13783 09-AUG-2001;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="MAP TO AC009225.1
                     EXPRESSED IN BRAIN, SIGNAL = 0.86
                     NT HIT: gi4501912, EVALUE 2.00e-28
                     EST_HUMAN HIT: AA091091.1, EVALUE 7.90e-01"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 6;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 ATAGAGCCACTAG 28
              |||||||||||||
Db         58 ATAGAGCCACTAG 46


RESULT 8
AR574640
LOCUS       AR574640                  19 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 3968 from patent US 6770633.
ACCESSION   AR574640
```

```
VERSION     AR574640.1  GI:56575532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: US 6770633-A 3968 03-AUG-2004;
            Immusol, Inc.; San Diego, CA
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          8 GTTACCATAGAG 19


RESULT 9
AR574641
LOCUS       AR574641                  19 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 3969 from patent US 6770633.
ACCESSION   AR574641
VERSION     AR574641.1  GI:56575533
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: US 6770633-A 3969 03-AUG-2004;
            Immusol, Inc.; San Diego, CA
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          7 GTTACCATAGAG 18


RESULT 10
AR574642
LOCUS       AR574642                  19 bp    DNA     linear   PAT 14-DEC-2004
DEFINITION  Sequence 3970 from patent US 6770633.
ACCESSION   AR574642
VERSION     AR574642.1  GI:56575534
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: US 6770633-A 3970 03-AUG-2004;
            Immusol, Inc.; San Diego, CA
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          2 GTTACCATAGAG 13


RESULT 11
AX132750
LOCUS       AX132750                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3968 from Patent WO0130362.
ACCESSION   AX132750
VERSION     AX132750.1  GI:14139055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3968 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db          8 GTTACCATAGAG 19


RESULT 12
AX132751
LOCUS       AX132751                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3969 from Patent WO0130362.
ACCESSION   AX132751
VERSION     AX132751.1  GI:14139056
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3969 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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                     /note="PCNA HH ribozyme binding site"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
               ||||||||||||
Db          7 GTTACCATAGAG 18


RESULT 13
AX132752
LOCUS       AX132752                 19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 3970 from Patent WO0130362.
ACCESSION   AX132752
VERSION     AX132752.1  GI:14139057
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 3970 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="PCNA HH ribozyme binding site"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
               ||||||||||||
Db          2 GTTACCATAGAG 13


RESULT 14
CQ855710
LOCUS       CQ855710                 23 bp    RNA     linear   PAT 31-AUG-2004
DEFINITION  Sequence 9 from Patent EP1449538.
ACCESSION   CQ855710
VERSION     CQ855710.1  GI:51850578
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ullrich,A., Gschwind,A. and Hart,S.
  TITLE     Inhibition of TACE or amphiregulin for the modulation of EGF
            receptor signal transactivation
  JOURNAL   Patent: EP 1449538-A 9 25-AUG-2004;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
     misc_difference 22. .23
                     /note="dT
                     Description of Artificial Sequence:siRNA"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCACT 26
               ||||||||||||
Db          3 CATAGAGCCACT 14


RESULT 15
CQ867591
LOCUS       CQ867591                 23 bp    RNA     linear   PAT 13-SEP-2004
DEFINITION  Sequence 9 from Patent WO2004073734.
ACCESSION   CQ867591
VERSION     CQ867591.1  GI:51997792
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ullrich,A., Gschwind,A. and Hart,S.
  TITLE     Inhibition of tace or amphiregulin for the modulation of egf
            receptor signal transactivation
  JOURNAL   Patent: WO 2004073734-A 9 02-SEP-2004;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
     misc_difference 22. .23
                     /note="dT
                     Description of Artificial Sequence:siRNA"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCACT 26
               ||||||||||||
Db          3 CATAGAGCCACT 14


Search completed: March  6, 2006, 00:38:42
Job time : 1170.5 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:21:59 ; Search time 360 Seconds
(without alignments)
666.144 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 11

Total number of hits satisfying chosen parameters: 11327990

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	29	100.0	29	8	US-10-720-424B-1	Sequence 1, Appli
	2	15	51.7	25	8	US-10-719-900-207943	Sequence 207943,
	3	15	51.7	25	8	US-10-719-900-473578	Sequence 473578,
	4	15	51.7	25	8	US-10-719-900-493325	Sequence 493325,
	5	15	51.7	25	10	US-11-036-317-670021	Sequence 670021,
c	6	14	48.3	25	5	US-10-098-263B-16386	Sequence 16386, A
c	7	14	48.3	25	7	US-10-719-956-350520	Sequence 350520,
	8	13	44.8	13	8	US-10-257-017B-176713	Sequence 176713,
c	9	13	44.8	13	8	US-10-257-017B-176714	Sequence 176714,
	10	13	44.8	17	3	US-09-927-046-382	Sequence 382, App
	11	13	44.8	17	3	US-09-927-046-1794	Sequence 1794, Ap
	12	13	44.8	17	3	US-09-927-046-2111	Sequence 2111, Ap
	13	13	44.8	24	8	US-10-720-424B-5	Sequence 5, Appli
c	14	13	44.8	25	7	US-10-681-773-3553	Sequence 3553, Ap
c	15	13	44.8	25	7	US-10-681-773-60170	Sequence 60170, A
c	16	13	44.8	25	7	US-10-681-773-87785	Sequence 87785, A
c	17	13	44.8	25	7	US-10-681-773-98759	Sequence 98759, A
c	18	13	44.8	25	7	US-10-681-773-99269	Sequence 99269, A
c	19	13	44.8	25	7	US-10-719-956-16054	Sequence 16054, A
c	20	13	44.8	25	7	US-10-719-956-290994	Sequence 290994,
c	21	13	44.8	25	7	US-10-719-956-533125	Sequence 533125,
c	22	13	44.8	25	8	US-10-719-900-350776	Sequence 350776,
c	23	13	44.8	25	8	US-10-719-900-375428	Sequence 375428,
c	24	13	44.8	25	8	US-10-719-900-453770	Sequence 453770,
c	25	13	44.8	25	8	US-10-719-900-919771	Sequence 919771,
	26	13	44.8	25	9	US-10-956-157-117633	Sequence 117633,
	27	13	44.8	25	9	US-10-956-157-117638	Sequence 117638,
	28	13	44.8	25	9	US-10-956-157-117639	Sequence 117639,
	29	13	44.8	25	9	US-10-956-157-223019	Sequence 223019,
c	30	13	44.8	25	9	US-10-956-157-224989	Sequence 224989,
c	31	13	44.8	25	9	US-10-843-527-79313	Sequence 79313, A
	32	13	44.8	25	9	US-10-843-527-158864	Sequence 158864,
c	33	13	44.8	25	10	US-11-036-317-759047	Sequence 759047,
	34	13	44.8	25	10	US-11-060-756-35453	Sequence 35453, A
	35	13	44.8	25	10	US-11-060-756-35457	Sequence 35457, A
	36	13	44.8	25	10	US-11-060-756-35481	Sequence 35481, A
c	37	13	44.8	25	10	US-11-060-756-57112	Sequence 57112, A
c	38	13	44.8	25	10	US-11-060-756-57116	Sequence 57116, A
c	39	13	44.8	25	10	US-11-060-756-57117	Sequence 57117, A
c	40	13	44.8	25	10	US-11-060-756-57119	Sequence 57119, A
c	41	13	44.8	25	10	US-11-060-756-294352	Sequence 294352,
	42	13	44.8	41	3	US-09-757-207-1	Sequence 1, Appli
	43	13	44.8	46	6	US-10-294-957-21	Sequence 21, Appl
	44	12	41.4	17	3	US-09-927-046-383	Sequence 383, App
	45	12	41.4	17	3	US-09-927-046-1572	Sequence 1572, Ap

ALIGNMENTS

RESULT 1
US-10-720-424B-1
; Sequence 1, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-1

Query Match 100.0%; Score 29; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GATGGTGATATGGTAGATACAGGATTTGG 29
              |||||||||||||||||||||||||||||
Db          1 GATGGTGATATGGTAGATACAGGATTTGG 29
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RESULT 2
US-10-719-900-207943
; Sequence 207943, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1

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;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 207943
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-207943

  Query Match             51.7%;  Score 15;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTAGATACAGGATTT 27
              |||||||||||||||
Db          2 GTAGATACAGGATTT 16


RESULT 3
US-10-719-900-473578
; Sequence 473578, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 473578
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-473578

  Query Match             51.7%;  Score 15;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTAGATACAGGATTT 27
              |||||||||||||||
Db          5 GTAGATACAGGATTT 19


RESULT 4
US-10-719-900-493325
; Sequence 493325, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
;  FILE REFERENCE: 3528.1
;  CURRENT APPLICATION NUMBER: US/10/719,900
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,808
;  PRIOR FILING DATE: 2002 11 20
;  NUMBER OF SEQ ID NOS: 982914
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493325
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-719-900-493325

  Query Match             51.7%;  Score 15;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTAGATACAGGATTT 27
              |||||||||||||||
Db          3 GTAGATACAGGATTT 17


RESULT 5
US-11-036-317-670021
; Sequence 670021, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
;  APPLICANT: Williams, Alan
;  APPLICANT:  Blume, John
;  TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
;  FILE REFERENCE: 3654.1
;  CURRENT APPLICATION NUMBER: US/11/036,317
;  CURRENT FILING DATE:  2005-01-13
;  PRIOR APPLICATION NUMBER: US 60/536,639
;  PRIOR FILING DATE: 2004-01-13
;  NUMBER OF SEQ ID NOS: 991174
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 670021
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-036-317-670021

  Query Match             51.7%;  Score 15;  DB 10;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GATATGGTAGATACA 21
              |||||||||||||||
Db         11 GATATGGTAGATACA 25


RESULT 6
US-10-098-263B-16386/c
; Sequence 16386, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
;  APPLICANT: Mittman, Michael
;  TITLE OF INVENTION: Human Microarray
;  FILE REFERENCE: 3118.1
;  CURRENT APPLICATION NUMBER: US/10/098,263B
;  CURRENT FILING DATE:  2003-01-08
;  PRIOR APPLICATION NUMBER: 60/276,759
;  PRIOR FILING DATE: 2001-03-16
;  NUMBER OF SEQ ID NOS: 131066
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16386
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-098-263B-16386

  Query Match             48.3%;  Score 14;  DB 5;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAGG 23
              ||||||||||||||
Db         25 ATGGTAGATACAGG 12


RESULT 7
US-10-719-956-350520/c
; Sequence 350520, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
;  APPLICANT: Xue Mei Zhou
;  TITLE OF INVENTION: Methods of Genetic Analysis of Rat
;  FILE REFERENCE: 3527.1
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; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 350520
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-350520

Query Match 48.3%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGTGATATGGTAGA 17
||||||||||||||
Db 18 GGTGATATGGTAGA 5

RESULT 8
US-10-257-017B-176713
; Sequence 176713, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 176713
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043853
US-10-257-017B-176713

Query Match 44.8%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGTGATATGGTAG 16
|||||||||||||
Db 1 GGTGATATGGTAG 13

RESULT 9
US-10-257-017B-176714/c
; Sequence 176714, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorhphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 176714
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0043853
US-10-257-017B-176714

Query Match 44.8%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GGTGATATGGTAG 16
|||||||||||||
Db 13 GGTGATATGGTAG 1

RESULT 10
US-09-927-046-382
; Sequence 382, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 382
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-382

Query Match 44.8%; Score 13; DB 3; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ATGGTAGATACAG 22
|:||:|||:||||
Db 4 AUGGUAGAUACAG 16

RESULT 11
US-09-927-046-1794
; Sequence 1794, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlor
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1794
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1794

Query Match 44.8%; Score 13; DB 3; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          2 AUGGUAGAUACAG 14
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RESULT 12
US-09-927-046-2111
; Sequence 2111, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2111
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-2111

Query Match 44.8%; Score 13; DB 3; Length 17;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          3 AUGGUAGAUACAG 15
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RESULT 13
US-10-720-424B-5
; Sequence 5, Application US/10720424B
; Publication No. US20040248085A1
; GENERAL INFORMATION:
; APPLICANT: ALBIOMED CO., LTD
; APPLICANT: Lee, Sang-Wha
; APPLICANT: Kim, Yeon-Soo
; APPLICANT: Yu, Kang-Yeol
; APPLICANT: Kim, Seung-Jo
; APPLICANT: Cha, Kwang-Yul
; APPLICANT: Ko, Jung-Jae
; TITLE OF INVENTION: GENERAL PRIMERS AND PROCESS FOR DETECTING DIVERSE GENOTYPES OF
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS BY PCR
; FILE REFERENCE: NEIT0018
; CURRENT APPLICATION NUMBER: US/10/720,424B
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: KR10-2002-0075370
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: KR10-2003-0053147
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human Papillomavirus
US-10-720-424B-5

Query Match 44.8%; Score 13; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 ATACAGGATTTGG 29
              |||||||||||||
Db         12 ATACAGGATTTGG 24
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RESULT 14
US-10-681-773-3553/c
; Sequence 3553, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-3553

Query Match 44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         15 AGATACAGGATTT 27
              |||||||||||||
Db         13 AGATACAGGATTT 1
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RESULT 15
US-10-681-773-60170/c
; Sequence 60170, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 60170
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-60170

Query Match 44.8%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         15 AGATACAGGATTT 27
              |||||||||||||
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Db 19 AGATACAGGATTT 7

Search completed: March 5, 2006, 23:01:34
Job time : 361 secs

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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:20:14 ; Search time 2987.5 Seconds
(without alignments)
454.167 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 1

Total number of hits satisfying chosen parameters: 777740

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14	48.3	74	9	AZ576177	AZ576177 AST-TD1.1
c	2	13	44.8	55	11	CR260472	CR260472 Forward s
	3	13	44.8	66	9	BZ291460	BZ291460 SALK_1207
c	4	13	44.8	83	2	BG932614	BG932614 h81-64 h8
	5	13	44.8	85	9	AZ919663	AZ919663 1006016B0
c	6	13	44.8	99	6	CB274455	CB274455 mai69c08.
c	7	13	44.8	100	7	CN563098	CN563098 taf83b02.
c	8	12	41.4	41	7	CO740007	CO740007 S1LB06a25
	9	12	41.4	43	10	CZ911033	CZ911033 4012004G0
c	10	12	41.4	46	7	CO735002	CO735002 S1LE04c10
	11	12	41.4	46	9	BH864657	BH864657 SALK_0965
c	12	12	41.4	52	11	CR357756	CR357756 Arabidops
c	13	12	41.4	53	9	B02637	B02637 cSRL-157G6-
c	14	12	41.4	54	9	AZ345736	AZ345736 1M0080M03
	15	12	41.4	61	1	AA585225	AA585225 KTH167 HT
c	16	12	41.4	61	9	AZ829961	AZ829961 2M0107I22
c	17	12	41.4	64	1	AI289007	AI289007 ql86h06.x
c	18	12	41.4	64	3	BM285347	BM285347 pb12g06.y
	19	12	41.4	66	1	AV770608	AV770608 AV770608
c	20	12	41.4	69	9	AZ767038	AZ767038 1M0566B01
c	21	12	41.4	70	3	BP916081	BP916081 BP916081
c	22	12	41.4	71	10	CG522729	CG522729 OST92796
	23	12	41.4	72	9	AZ665106	AZ665106 1M0545C24
c	24	12	41.4	73	6	CD398050	CD398050 Gm_ck1911
c	25	12	41.4	73	10	AG251154	AG251154 Lotus cor
	26	12	41.4	78	1	AV956811	AV956811 AV956811
c	27	12	41.4	79	9	AZ345739	AZ345739 1M0080M06
	28	12	41.4	86	7	CN857089	CN857089 000722AAA
c	29	12	41.4	87	9	BH186923	BH186923 032_P_09-
	30	12	41.4	87	10	CG577082	CG577082 OST212495
c	31	12	41.4	87	11	CNS07RAJ	AL623869 T7 end of
	32	12	41.4	90	5	BU653687	BU653687 1112108C1
	33	12	41.4	90	6	CD944463	CD944463 RDI_67 Ge
c	34	12	41.4	90	10	CL436082	CL436082 PST2274-N
	35	12	41.4	96	9	BH853741	BH853741 SALK_0781
	36	12	41.4	99	3	BP048125	BP048125 BP048125
c	37	12	41.4	99	5	BU822313	BU822313 UB35DPE01
c	38	12	41.4	99	10	CG620161	CG620161 OST316914
c	39	12	41.4	100	1	AW179280	AW179280 CM2-ST009
	40	12	41.4	100	1	AW899633	AW899633 RC4-NN008
	41	12	41.4	100	8	CX054323	CX054323 tai97h03.
	42	12	41.4	100	9	AZ791784	AZ791784 2M0041O16
c	43	11	37.9	29	11	TA196C12P	AL475923 T. brucei
c	44	11	37.9	30	10	CZ487828	CZ487828 f05203-3p
	45	11	37.9	31	1	AI377540	AI377540 tc15g07.x

ALIGNMENTS

RESULT 1
AZ576177/c
LOCUS AZ576177 74 bp DNA linear GSS 06-DEC-2000
DEFINITION AST-TD1.1SD-73 Genetrap T47D Human Breast Carcinoma Library Homo sapiens genomic 5', genomic survey sequence.
ACCESSION AZ576177
VERSION AZ576177.1 GI:11562488
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 74)
AUTHORS Henkel,G., Liyanage,M., Pratt,E., Huang,D., Riley,M., Bernardino,A., Durick,K. and Pollok,B.
TITLE Exon-trap tags from a T47D GenomeScreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkelg@aurorabio.com
Pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAmp-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.
Class: exon-trapped.
FEATURES Location/Qualifiers
source 1. .74
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"

/note="Organ: Breast; Vector: pAmp-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAmp-1 and used to transform DH5-alpha competent bacteria."

ORIGIN

Query Match 48.3%; Score 14; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GATATGGTAGATAC 20
||||||||||||||
Db 63 GATATGGTAGATAC 50

RESULT 2
CR260472/c
LOCUS CR260472 55 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN342d22, genomic survey sequence.
ACCESSION CR260472
VERSION CR260472.1 GI:50039325
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 55)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES Location/Qualifiers
source 1. .55
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN342d22"
/clone_lib="MHPN"

ORIGIN

Query Match 44.8%; Score 13; DB 11; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ATGGTAGATACAG 22
|||||||||||||
Db 15 ATGGTAGATACAG 3

RESULT 3
BZ291460
LOCUS BZ291460 66 bp DNA linear GSS 24-OCT-2002
DEFINITION SALK_120782.34.65.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_120782.34.65.x, genomic survey sequence.
ACCESSION BZ291460
VERSION BZ291460.1 GI:24336973
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 66)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At3g47220.
Class: TDNA tagged.
FEATURES Location/Qualifiers
source 1. .66
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_120782.34.65.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 44.8%; Score 13; DB 9; Length 66;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TGGTGATATGGTA 15
|||||||||||||
Db 29 TGGTGATATGGTA 41

RESULT 4
BG932614/c
LOCUS BG932614 83 bp mRNA linear EST 03-JUL-2002
DEFINITION h81-64 h81 S. mansoni adult mini-library, Fietto/DeMarco/Verjovski-Almeida Schistosoma mansoni cDNA, mRNA sequence.
ACCESSION BG932614
VERSION BG932614.1 GI:17157567
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 83)
AUTHORS Fietto,J.L.R., DeMarco,R. and Verjovski-Almeida,S.
TITLE Use of degenerate primers and touchdown PCR for construction of cDNA libraries
JOURNAL Biotechniques 32 (6), 1404-1408 (2002)
PUBMED 12074173
COMMENT Contact: Verjovski-Almeida S
Departmento de Bioquimica, Instituto de Quimica
Universidade de Sao Paulo
Av. Lineu Prestes, 748, Sao Paulo, SP 05508-900, Brasil
Tel: 55-11-3091-2173
Fax: 55-11-3091-2186
Email: verjo@iq.usp.br.
FEATURES Location/Qualifiers
source 1. .83
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/strain="BH"
/db_xref="taxon:6183"
/dev_stage="Adult"
/clone_lib="h81 S. mansoni adult mini-library, Fietto/DeMarco/Verjovski-Almeida"
/note="Vector: Bluescript SK; minilibrary constructed using low-stringency RT-PCR and consensus-degenerate primer"

```
ORIGIN

  Query Match             44.8%;  Score 13;  DB 2;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 ATACAGGATTTGG 29
              |||||||||||||
Db         13 ATACAGGATTTGG 1


RESULT 5
AZ919663
LOCUS       AZ919663                  85 bp    DNA     linear   GSS 17-DEC-2001
DEFINITION  1006016B04.x1 1006 - RescueMu Grid G Zea mays genomic, genomic
            survey sequence.
ACCESSION   AZ919663
VERSION     AZ919663.1  GI:13389597
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1006016  row: 41
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="1006 - RescueMu Grid G"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
                     extracted from leaf punches, double digested using BamHI
                     and BglII, and ligated to form circular plasmids. DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
ORIGIN

  Query Match             44.8%;  Score 13;  DB 9;  Length 85;
  Best Local Similarity   100.0%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 ATGGTAGATACAG 22
              |||||||||||||
Db          6 ATGGTAGATACAG 18


RESULT 6
CB274455/c
LOCUS       CB274455                  99 bp    mRNA    linear   EST 24-FEB-2003
DEFINITION  mai69c08.y1 McCarrey Eddy spermatocytes Mus musculus cDNA clone
            IMAGE:6446702 5', mRNA sequence.
ACCESSION   CB274455
VERSION     CB274455.1  GI:28464778
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 99)
  AUTHORS   McCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
            Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
            Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
            Bennett,J., Waterston,R. and Wilson,R.
  TITLE     NIEHS Mouse
  JOURNAL   Unpublished (2002)
COMMENT     Contact: McCarrey/Eddy NIEHS Mouse
            NIEHS Mouse
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed and donated by J. McCarrey, Ph.D. (Southwest
            Foundation for Biomedical Research, Dept. of Genetics) - excision
            done by E.M. Eddy, Ph.D. (National Institutes of Health, National
            Institute of Environmental Health Sciences).
            MGI:2070662
            Seq primer: Primer name ambiguous.
FEATURES             Location/Qualifiers
     source          1. .99
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CD-1"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6446702"
                     /sex="male"
                     /tissue_type="spermatocytes, pooled from multiple mice"
                     /dev_stage="60 day"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="McCarrey Eddy spermatocytes"
                     /note="Organ: testis; Vector: pBluescript SK+
                     (Stratagene); Site_1: XhoI; Site_2: EcoRI; cDNA oligo
                     dT-primed [5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTT-3'] and
                     directionally cloned  using 5' linkers 5'-AATTCGGCACGAG-3'
                     and 5'-CTCGTGCCG-3'. Size selection of >400bp material
                     gives average insert size ranging from 1-2 kb. Library was
                     mass excised (from  lambda-UniZAP-XR) and resulting
                     single-stranded phagemids were prepped and tranformed
                     into DH10B. Library contains 98% recombinants.
                     References: J. Androl. 20:635-639 and Gene 25:263-269.
                     Library constructed and donated by J. McCarrey, Ph.D.
                     (Southwest Foundation for Biomedical Research, Dept. of
                     Genetics); excision done by E.M. Eddy, Ph.D. (National
                     Institutes of  Health, National Institute of Environmental
                     Health Sciences). Original lambda-based library is
                     available through ATCC, catalog #63422."
ORIGIN

  Query Match             44.8%;  Score 13;  DB 6;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TGGTGATATGGTA 15
              |||||||||||||
Db         62 TGGTGATATGGTA 50


RESULT 7
CN563098/c
LOCUS       CN563098                 100 bp    mRNA    linear   EST 03-MAY-2004
DEFINITION  taf83b02.x2 Hydra EST -Kiel 1 Hydra magnipapillata cDNA 3' similar
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```
            to SW:RLA2_BRAFL O01725 60S ACIDIC RIBOSOMAL PROTEIN P2. ;, mRNA
            sequence.
ACCESSION   CN563098
VERSION     CN563098.1  GI:46972402
KEYWORDS    EST.
SOURCE      Hydra magnipapillata
  ORGANISM  Hydra magnipapillata
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
            Hydridae; Hydra.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
            Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M.,
            Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y.,
            Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R.,
            Maguire,L., Kennedy,S., Waterston,R. and Wilson,R.
  TITLE     WashU Hydra EST Project
  JOURNAL   Unpublished (2002)
COMMENT     Other_ESTs: taf83b02.y2
            Contact: Hans Bode
            WashU Hydra EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by Konstantin Khalturin, Zoologisches
            Institut, Univ. Kiel, Germany Library materials provided by Thomas
            Bosch, Zoologisches Institut, CAU Kiel, Germany DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
            Putative full length read
            vector to vector length is
            Seq primer: degenerate primer.
FEATURES             Location/Qualifiers
     source          1. .100
                     /organism="Hydra magnipapillata"
                     /mol_type="mRNA"
                     /strain="105"
                     /db_xref="taxon:6085"
                     /lab_host="DH5a"
                     /clone_lib="Hydra EST -Kiel 1"
                     /note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I;
                     pSPORT 1 Vector is ampicillin resistent, M13 reverse
                     primer was used by us for sequencing of 5' parts of
                     inserts; 3' parts of cDNAs contain long polyA tracks which
                     makes sequencing from 3' direction complicated"
ORIGIN

  Query Match             44.8%;  Score 13;  DB 7;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGG 13
              |||||||||||||
Db         27 GATGGTGATATGG 15


RESULT 8
CO740007/c
LOCUS       CO740007                  41 bp    mRNA    linear   EST 29-JUL-2004
DEFINITION  S1LB06a25l03f1 squirrel brain library 1 Spermophilus lateralis cDNA
            clone 25l03 5', mRNA sequence.
ACCESSION   CO740007
VERSION     CO740007.1  GI:50827277
KEYWORDS    EST.
SOURCE      Spermophilus lateralis (golden-mantled ground squirrel)
  ORGANISM  Spermophilus lateralis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
            Rogers,J. and Cossins,A.R.
  TITLE     Microarray analysis of transcriptional changes during hibernation
            in the golden mantled ground squirrel, Spermophilus lateralis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 25  row: 1  column: 03
            Seq primer: TriplEx 5'LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3')
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Spermophilus lateralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:76772"
                     /clone="25l03"
                     /sex="Male & female"
                     /tissue_type="brain"
                     /dev_stage="Adult"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel brain library 1"
                     /note="Vector: pTriplEx2; Site_1: Sfi1 GGCCATTACGGCC;
                     Site_2: Sfi1 GGCCGCCTCGGCC; Normalized cDNA library
                     prepared from brain of hibernating and summer animals"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 7;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GGTGATATGGTA 15
              ||||||||||||
Db         14 GGTGATATGGTA 3


RESULT 9
CZ911033
LOCUS       CZ911033                  43 bp    DNA     linear   GSS 08-AUG-2005
DEFINITION  4012004G06.2EL_y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
            survey sequence.
ACCESSION   CZ911033
VERSION     CZ911033.1  GI:71925177
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 4012004  column: 2
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73/K55"
```

```
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="4012 - RescueMu Grid BB"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'http://www.mutransposon.org/project/RescueMu/'. Grid
                     BB was grown at UC Berkeley in 2001. DNA was extracted
                     from leaf strips, double digested using BamHI and BglII,
                     and ligated to form circular plasmids. DH10B cells were
                     transformed and then screened on LB plates with
                     ampicillin."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 10;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TGGTAGATACAG 22
               ||||||||||||
Db          32 TGGTAGATACAG 43


RESULT 10
CO735002/c
LOCUS       CO735002                 46 bp    mRNA    linear   EST 29-JUL-2004
DEFINITION  S1LE04c10g02f1 squirrel embryo library 1 Spermophilus lateralis
            cDNA clone 10g02 5', mRNA sequence.
ACCESSION   CO735002
VERSION     CO735002.1  GI:50822272
KEYWORDS    EST.
SOURCE      Spermophilus lateralis (golden-mantled ground squirrel)
  ORGANISM  Spermophilus lateralis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
            Rogers,J. and Cossins,A.R.
  TITLE     Microarray analysis of transcriptional changes during hibernation
            in the golden mantled ground squirrel, Spermophilus lateralis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 10  row: g  column: 02
            Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
            High quality sequence stop: 46.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Spermophilus lateralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:76772"
                     /clone="10g02"
                     /sex="male and female"
                     /tissue_type="embryo"
                     /dev_stage="embryonic"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel embryo library 1"
                     /note="Vector: pFLC; Site_1: SalI GTCGAG; Site_2: BamHI
                     GGATCC; Normalized and subtracted cDNA library prepared
                     from embryos"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 7;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GTAGATACAGGA 24
               ||||||||||||
Db          17 GTAGATACAGGA 6


RESULT 11
BH864657
LOCUS       BH864657                 46 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_096549 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_096549, genomic survey sequence.
ACCESSION   BH864657
VERSION     BH864657.1  GI:22100555
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At1g79990.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_096549"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 9;  Length 46;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 GTAGATACAGGA 24
               ||||||||||||
Db          19 GTAGATACAGGA 30


RESULT 12
CR357756/c
LOCUS       CR357756                 52 bp    DNA     linear   GSS 05-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-722B11-025198,
            genomic survey sequence.
ACCESSION   CR357756
VERSION     CR357756.1  GI:45540678
```

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 52)
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F9D24. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .52
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-722B11-025198"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGABI1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN

Query Match 41.4%; Score 12; DB 11; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ATGGTAGATACA 21
||||||||||||
Db 34 ATGGTAGATACA 23

RESULT 13
B02637/c
LOCUS B02637 53 bp DNA linear GSS 13-JUL-1996
DEFINITION cSRL-157G6-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-157G6, genomic survey sequence.
ACCESSION B02637
VERSION B02637.1 GI:1411915
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 53)
AUTHORS Evans,G.A., Burbee,D., Davies,C., Hahner,L., Oliver,T., Gilbert,M., Jones,D., Ward,T., Gillilan,E., Schagemann,J., Probst,S. ., Harris,J., DeFord,J., McFarland,J., Burzinski,K., Khan,M., Kupfer,K. and Garner,H.R.
TITLE Genomic Sequence Sampled Map of Chromosome 11
JOURNAL Unpublished (1996)
COMMENT Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At Dallas
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
Email: gevans@utsw.swmed.edu, shane@mcdermott.swmed.edu
Seq primer: T7
Class: cosmid ends
High quality sequence stop: 53.
FEATURES Location/Qualifiers
source 1. .53
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="cSRL-157G6"
/sex="female"
/cell_type="chimeric hamster somatic cell hybrid"
/clone_lib="cSRL flow sorted Chromosome 11 specific cosmid"
/note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hampster Ovary (CHO) monochromosomal somatic cell hybrid, J1"
ORIGIN

Query Match 41.4%; Score 12; DB 9; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TAGATACAGGAT 25
||||||||||||
Db 17 TAGATACAGGAT 6

RESULT 14
AZ345736/c
LOCUS AZ345736 54 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080M03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080M03 R, genomic survey sequence.
ACCESSION AZ345736
VERSION AZ345736.1 GI:10424973
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 54)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

```
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: M  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 54.
FEATURES              Location/Qualifiers
     source           1. .54
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC1M0080M03"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 9;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGATATGGTAGA 17
              ||||||||||||
Db         23 TGATATGGTAGA 12


RESULT 15
AA585225
LOCUS       AA585225                 61 bp    mRNA    linear   EST 09-SEP-1997
DEFINITION  KTH167 HTCDL1 Homo sapiens cDNA 5'/3', mRNA sequence.
ACCESSION   AA585225
VERSION     AA585225.1  GI:2385113
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 61)
  AUTHORS   Sohn,U., Park,D.S., Lee,C.M., Cho,W.K., Ahn,H.J., Lee,M.Y.,
            Hwang,M.Y. and Jin,S.W.
  TITLE     Human HTCDL1 library cDNAs
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Uik
            Sohn,D.S.Park,C.M.Lee,W.K.Cho,H.J.Ahn,M.Y.Lee,M.Y.Hwang,S.W.Jin
            Laboratory of Molecular Biology
            Kyungpook National University
            Dept. of Genetic Eng.,Kyungpook National Univ., Taegu 702-701,
            Korea
            Tel: 82-053-950-5382
            Fax: 82-053-955-5327
            Email: usohn@bh.kyungpook.ac.kr
            Seq primer: M13 Reverse/SK primer.
FEATURES              Location/Qualifiers
     source           1. .61
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /lab_host="XL1-Blue"
                      /clone_lib="HTCDL1"
                      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                      EcoRI; Poly(A)-mRNA  from the  2-year  old male  fetal
                      thymus, oligo(dT)  priming,  EcoRI cloning in the vector
                      pBluescipt (Stratagene)."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 1;  Length 61;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GTGATATGGTAG 16
              ||||||||||||
Db         21 GTGATATGGTAG 32


Search completed: March  6, 2006, 00:16:49
Job time : 2991.5 secs
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:22:58 ; Search time 449.5 Seconds
(without alignments)
141.451 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7218535 seqs, 1096242582 residues

Word size : 4

Total number of hits satisfying chosen parameters: 11882884

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	48.3	18	8	US-10-310-914A-927774	Sequence 927774,
	2	14	48.3	19	10	US-11-101-244-1492736	Sequence 1492736,
	3	14	48.3	19	11	US-11-083-784-1492736	Sequence 1492736,
c	4	14	48.3	25	12	US-11-121-849-276816	Sequence 276816,
	5	14	48.3	50	12	US-11-175-859-93016	Sequence 93016, A
	6	13	44.8	19	10	US-11-101-244-662756	Sequence 662756,
	7	13	44.8	19	10	US-11-101-244-662769	Sequence 662769,
c	8	13	44.8	19	10	US-11-101-244-1366068	Sequence 1366068,
	9	13	44.8	19	10	US-11-101-244-1379350	Sequence 1379350,
	10	13	44.8	19	10	US-11-101-244-1492657	Sequence 1492657,
	11	13	44.8	19	11	US-11-083-784-662756	Sequence 662756,
	12	13	44.8	19	11	US-11-083-784-662769	Sequence 662769,
c	13	13	44.8	19	11	US-11-083-784-1366068	Sequence 1366068,
	14	13	44.8	19	11	US-11-083-784-1379350	Sequence 1379350,
	15	13	44.8	19	11	US-11-083-784-1492657	Sequence 1492657,
	16	13	44.8	21	7	US-10-537-002-67	Sequence 67, Appl
c	17	13	44.8	25	12	US-11-121-849-384840	Sequence 384840,
c	18	13	44.8	25	12	US-11-121-849-385027	Sequence 385027,
c	19	13	44.8	25	12	US-11-121-849-480659	Sequence 480659,
c	20	13	44.8	25	12	US-11-121-849-512932	Sequence 512932,
	21	13	44.8	25	12	US-11-121-849-581818	Sequence 581818,
c	22	13	44.8	26	8	US-10-310-914A-216214	Sequence 216214,
	23	13	44.8	42	7	US-10-991-285-861	Sequence 861, App
c	24	13	44.8	50	12	US-11-175-859-7946	Sequence 7946, Ap
c	25	13	44.8	50	12	US-11-175-859-29991	Sequence 29991, A
	26	13	44.8	50	12	US-11-175-859-50688	Sequence 50688, A
	27	13	44.8	50	12	US-11-175-859-85087	Sequence 85087, A
c	28	13	44.8	50	12	US-11-175-859-110204	Sequence 110204,
c	29	12	41.4	18	8	US-10-310-914A-115918	Sequence 115918,
c	30	12	41.4	18	8	US-10-310-914A-474057	Sequence 474057,
c	31	12	41.4	19	10	US-11-101-244-73600	Sequence 73600, A
	32	12	41.4	19	10	US-11-101-244-259581	Sequence 259581,
	33	12	41.4	19	10	US-11-101-244-343861	Sequence 343861,
	34	12	41.4	19	10	US-11-101-244-344879	Sequence 344879,
c	35	12	41.4	19	10	US-11-101-244-356787	Sequence 356787,
	36	12	41.4	19	10	US-11-101-244-530085	Sequence 530085,
	37	12	41.4	19	10	US-11-101-244-530127	Sequence 530127,
	38	12	41.4	19	10	US-11-101-244-530128	Sequence 530128,
	39	12	41.4	19	10	US-11-101-244-653539	Sequence 653539,
	40	12	41.4	19	10	US-11-101-244-698032	Sequence 698032,
	41	12	41.4	19	10	US-11-101-244-698151	Sequence 698151,
c	42	12	41.4	19	10	US-11-101-244-752005	Sequence 752005,
c	43	12	41.4	19	10	US-11-101-244-752057	Sequence 752057,
c	44	12	41.4	19	10	US-11-101-244-777350	Sequence 777350,
c	45	12	41.4	19	10	US-11-101-244-777367	Sequence 777367,

ALIGNMENTS

RESULT 1
US-10-310-914A-927774
; Sequence 927774, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 927774
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-927774

Query Match 48.3%; Score 14; DB 8; Length 18;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GGTGATATGGTAGA 17
              ||:||:|:||:|||
Db          1 GGUGAUAUGGUAGA 14
```

RESULT 2
US-11-101-244-1492736
; Sequence 1492736, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244

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;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1492736
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1492736

  Query Match             48.3%;  Score 14;  DB 10;  Length 19;
  Best Local Similarity   78.6%;  Pred. No. 85;
  Matches   11;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGTAGATACAGGAT 25
              ||:|||:||||||:
Db          4 GGUAGAUACAGGAU 17


RESULT 3
US-11-083-784-1492736
; Sequence 1492736, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1492736
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1492736

  Query Match             48.3%;  Score 14;  DB 11;  Length 19;
  Best Local Similarity   78.6%;  Pred. No. 85;
  Matches   11;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGTAGATACAGGAT 25
              ||:|||:||||||:
Db          4 GGUAGAUACAGGAU 17


RESULT 4
US-11-121-849-276816/c
; Sequence 276816, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;  APPLICANT: John Palma
;  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
;  TITLE OF INVENTION:  Microarrays
;  FILE REFERENCE: 3684.1
;  CURRENT APPLICATION NUMBER: US/11/121,849
;  CURRENT FILING DATE:  2005-05-03
;  PRIOR APPLICATION NUMBER: 60/567,949
;  PRIOR FILING DATE: 2004-05-03
;  NUMBER OF SEQ ID NOS: 673904
;  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 276816
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-276816

  Query Match             48.3%;  Score 14;  DB 12;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 86;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GGTGATATGGTAGA 17
              ||||||||||||||
Db         15 GGTGATATGGTAGA 2


RESULT 5
US-11-175-859-93016
; Sequence 93016, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
;  APPLICANT: Affymetrix, Inc.
;  APPLICANT:  Liu, Guoying et al.
;  TITLE OF INVENTION: Method of Analysis of Human Polymorphism
;  FILE REFERENCE: 3690.1
;  CURRENT APPLICATION NUMBER: US/11/175,859
;  CURRENT FILING DATE:  2005-07-05
;  PRIOR APPLICATION NUMBER: US 60/585,352
;  PRIOR FILING DATE: 2004-07-02
;  NUMBER OF SEQ ID NOS: 116251
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93016
;   LENGTH: 50
;   TYPE: DNA
;   ORGANISM: homo sapien
US-11-175-859-93016

  Query Match             48.3%;  Score 14;  DB 12;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 88;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGT 14
              ||||||||||||||
Db         30 GATGGTGATATGGT 43


RESULT 6
US-11-101-244-662756
; Sequence 662756, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 662756
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-662756
```

Query Match 44.8%; Score 13; DB 10; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          4 AUGGUAGAUACAG 16
```

RESULT 7
US-11-101-244-662769
; Sequence 662769, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 662769
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-662769

Query Match 44.8%; Score 13; DB 10; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy         10 ATGGTAGATACAG 22
              |:||:|||:||||
Db          5 AUGGUAGAUACAG 17
```

RESULT 8
US-11-101-244-1366068/c
; Sequence 1366068, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1366068
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1366068

Query Match 44.8%; Score 13; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 ATACAGGATTTGG 29
              |||||||||||||
Db         17 ATACAGGATTTGG 5
```

RESULT 9
US-11-101-244-1379350
; Sequence 1379350, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1379350
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1379350

Query Match 44.8%; Score 13; DB 10; Length 19;
Best Local Similarity 69.2%; Pred. No. 3.3e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 TAGATACAGGATT 26
              :|||:||||||::
Db          6 UAGAUACAGGAUU 18
```

RESULT 10
US-11-101-244-1492657
; Sequence 1492657, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492657
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1492657

Query Match 44.8%; Score 13; DB 10; Length 19;

Best Local Similarity 76.9%; Pred. No. 3.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          13 GTAGATACAGGAT 25
               |:|||:||||||:
Db           1 GUAGAUACAGGAU 13
```

RESULT 11
US-11-083-784-662756
; Sequence 662756, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 662756
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-662756

Query Match 44.8%; Score 13; DB 11; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          10 ATGGTAGATACAG 22
               |:||:|||:||||
Db           4 AUGGUAGAUACAG 16
```

RESULT 12
US-11-083-784-662769
; Sequence 662769, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 662769
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-662769

Query Match 44.8%; Score 13; DB 11; Length 19;
Best Local Similarity 76.9%; Pred. No. 3.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          10 ATGGTAGATACAG 22
               |:||:|||:||||
Db           5 AUGGUAGAUACAG 17
```

RESULT 13
US-11-083-784-1366068/c
; Sequence 1366068, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1366068
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1366068

Query Match 44.8%; Score 13; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          17 ATACAGGATTTGG 29
               |||||||||||||
Db          17 ATACAGGATTTGG 5
```

RESULT 14
US-11-083-784-1379350
; Sequence 1379350, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1379350

```
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1379350

  Query Match            44.8%;  Score 13;  DB 11;  Length 19;
  Best Local Similarity  69.2%;  Pred. No. 3.3e+02;
  Matches    9;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TAGATACAGGATT 26
              :|||:||||||::
Db          6 UAGAUACAGGAUU 18


RESULT 15
US-11-083-784-1492657
; Sequence 1492657, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1492657
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1492657

  Query Match            44.8%;  Score 13;  DB 11;  Length 19;
  Best Local Similarity  76.9%;  Pred. No. 3.3e+02;
  Matches   10;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 GTAGATACAGGAT 25
              |:|||:||||||:
Db          1 GUAGAUACAGGAU 13


Search completed: March  5, 2006, 22:48:29
Job time : 450.5 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 78 Seconds
(without alignments)
660.888 Million cell updates/sec

Title: US-10-720-424B-1
Perfect score: 29
Sequence: 1 gatggtgatatggtagatacaggatttgg 29

Scoring-table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word-size : 17

Total number of hits satisfying chosen parameters: 1426356

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	48.3	38	2	US-08-316-293-53	Sequence 53, Appl
	2	13	44.8	41	3	US-09-757-207-1	Sequence 1, Appli
	3	12	41.4	20	3	US-09-198-452A-3549	Sequence 3549, Ap
c	4	12	41.4	21	2	US-08-358-171-13	Sequence 13, Appl
c	5	12	41.4	21	3	US-09-090-947-13	Sequence 13, Appl
	6	12	41.4	25	3	US-09-396-196G-36348	Sequence 36348, A
c	7	12	41.4	25	3	US-09-396-196G-73518	Sequence 73518, A
c	8	12	41.4	25	3	US-09-396-196G-73519	Sequence 73519, A
c	9	12	41.4	25	3	US-09-396-196G-81905	Sequence 81905, A
c	10	12	41.4	25	3	US-09-396-196G-94653	Sequence 94653, A
c	11	12	41.4	25	3	US-09-396-196G-94664	Sequence 94664, A
c	12	12	41.4	25	3	US-09-396-196G-94665	Sequence 94665, A
	13	12	41.4	98	3	US-09-513-999C-22225	Sequence 22225, A
c	14	11	37.9	20	3	US-09-021-701-1077	Sequence 1077, Ap
c	15	11	37.9	20	3	US-09-021-701-1078	Sequence 1078, Ap
c	16	11	37.9	20	3	US-09-021-701-1079	Sequence 1079, Ap
c	17	11	37.9	20	3	US-09-021-701-1080	Sequence 1080, Ap
c	18	11	37.9	20	3	US-09-021-701-1081	Sequence 1081, Ap
c	19	11	37.9	20	3	US-09-021-701-1082	Sequence 1082, Ap
c	20	11	37.9	20	3	US-09-021-701-1083	Sequence 1083, Ap
c	21	11	37.9	20	3	US-09-021-701-1084	Sequence 1084, Ap
c	22	11	37.9	20	3	US-09-021-701-1085	Sequence 1085, Ap
c	23	11	37.9	20	3	US-09-021-701-1086	Sequence 1086, Ap
c	24	11	37.9	20	3	US-09-363-970-11	Sequence 11, Appl
c	25	11	37.9	20	3	US-09-198-452A-2044	Sequence 2044, Ap
	26	11	37.9	22	3	US-09-612-204B-30	Sequence 30, Appl
	27	11	37.9	22	3	US-10-055-364-30	Sequence 30, Appl
	28	11	37.9	24	3	US-08-828-952-2	Sequence 2, Appli
c	29	11	37.9	25	3	US-09-396-196G-32627	Sequence 32627, A
c	30	11	37.9	25	3	US-09-396-196G-32638	Sequence 32638, A
c	31	11	37.9	25	3	US-09-396-196G-32639	Sequence 32639, A
c	32	11	37.9	25	3	US-09-396-196G-32640	Sequence 32640, A
c	33	11	37.9	25	3	US-09-396-196G-32641	Sequence 32641, A
c	34	11	37.9	25	3	US-09-396-196G-43128	Sequence 43128, A
c	35	11	37.9	25	3	US-09-396-196G-43129	Sequence 43129, A
c	36	11	37.9	25	3	US-09-396-196G-73517	Sequence 73517, A
c	37	11	37.9	25	3	US-09-396-196G-120975	Sequence 120975,
c	38	11	37.9	25	3	US-09-396-196G-120976	Sequence 120976,
c	39	11	37.9	25	3	US-09-396-196G-120977	Sequence 120977,
c	40	11	37.9	25	3	US-09-396-196G-120978	Sequence 120978,
c	41	11	37.9	25	3	US-10-002-623-348	Sequence 348, App
	42	11	37.9	29	3	US-09-670-075A-8	Sequence 8, Appli
c	43	11	37.9	30	2	US-08-361-337-50	Sequence 50, Appl
	44	11	37.9	30	3	US-09-470-661A-38	Sequence 38, Appl
	45	11	37.9	32	2	US-07-931-473B-331	Sequence 331, App

ALIGNMENTS

RESULT 1
US-08-316-293-53
; Sequence 53, Application US/08316293
; Patent No. 5484699
; GENERAL INFORMATION:
; APPLICANT: ABBOTT LABORATORIES
; APPLICANT: Stanley R. Bouma
; APPLICANT: Thomas G. Laffler
; APPLICANT: Ronald L. Marshall
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES USEFUL AS
; TITLE OF INVENTION: TYPE-SPECIFIC PROBES, PCR PRIMERS AND LCR PROBES
; TITLE OF INVENTION: FOR THE AMPLIFICATION AND DETECTION OF HUMAN
; TITLE OF INVENTION: PAPILLOMA VIRUS, AND REALTED KITS AND METHODS.
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,293
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,665
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 4853.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 937-4884
; TELEFAX: (708) 937-9556
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)

```
US-08-316-293-53

  Query Match             48.3%;  Score 14;  DB 2;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GATGGTGATATGGT 14
              ||||||||||||||
Db          1 GATGGTGATATGGT 14


RESULT 2
US-09-757-207-1
; Sequence 1, Application US/09757207
; Patent No. 6770752
; GENERAL INFORMATION:
;  APPLICANT:  Hellyer, Tobin J.
;  APPLICANT:  You, Qimin
;  APPLICANT:  Harris, James M.
;  TITLE OF INVENTION:  Sequences and Methods for Detection of HIV-1
;  FILE REFERENCE:  Seq/Mtds for Detection of HIV-1
;  CURRENT APPLICATION NUMBER: US/09/757,207
;  CURRENT FILING DATE:  2001-01-09
;  NUMBER OF SEQ ID NOS:  37
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 41
;   TYPE: DNA
;   ORGANISM: Human immunodeficiency virus type 1
US-09-757-207-1

  Query Match             44.8%;  Score 13;  DB 3;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 GGTAGATACAGGA 24
              |||||||||||||
Db         23 GGTAGATACAGGA 35


RESULT 3
US-09-198-452A-3549
; Sequence 3549, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3549
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3549

  Query Match             41.4%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 GATACAGGATTT 27
              ||||||||||||
Db          2 GATACAGGATTT 13


RESULT 4
US-08-358-171-13/c
; Sequence 13, Application US/08358171
; Patent No. 5763578
;  GENERAL INFORMATION:
;    APPLICANT:  FONG, Henry K.W.
;    TITLE OF INVENTION:  ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
;    TITLE OF INVENTION:  ENCODING SAME, AND ANTIBODIES THERETO
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/358,171
;      FILING DATE:  16-DEC-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  FONG=2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-08-358-171-13

  Query Match             41.4%;  Score 12;  DB 2;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TAGATACAGGAT 25
              ||||||||||||
Db         13 TAGATACAGGAT 2


RESULT 5
US-09-090-947-13/c
; Sequence 13, Application US/09090947
; Patent No. 6008338
;  GENERAL INFORMATION:
;    APPLICANT:  FONG, Henry K.W.
;    TITLE OF INVENTION:  ALL TRANS-RETINALDEHYDE BINDING PROTEIN, DNA
;    TITLE OF INVENTION:  ENCODING SAME, AND ANTIBODIES THERETO
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/090,947
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/358,171
```

```
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  FONG=2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
US-09-090-947-13

  Query Match             41.4%;  Score 12;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TAGATACAGGAT 25
              ||||||||||||
Db         13 TAGATACAGGAT 2


RESULT 6
US-09-396-196G-36348
; Sequence 36348, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36348
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-36348

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 TGGTGATATGGT 14
              ||||||||||||
Db         11 TGGTGATATGGT 22


RESULT 7
US-09-396-196G-73518/c
; Sequence 73518, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73518
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-73518

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGATATGGTAGA 17
              ||||||||||||
Db         23 TGATATGGTAGA 12


RESULT 8
US-09-396-196G-73519/c
; Sequence 73519, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73519
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-73519

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 TGATATGGTAGA 17
              ||||||||||||
Db         20 TGATATGGTAGA 9


RESULT 9
US-09-396-196G-81905/c
; Sequence 81905, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81905
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-81905
```

Query Match 41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          13 GTAGATACAGGA 24
               ||||||||||||
Db          21 GTAGATACAGGA 10
```

RESULT 10
US-09-396-196G-94653/c
; Sequence 94653, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94653
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-94653

Query Match 41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           6 TGATATGGTAGA 17
               ||||||||||||
Db          23 TGATATGGTAGA 12
```

RESULT 11
US-09-396-196G-94664/c
; Sequence 94664, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-94664

Query Match 41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           6 TGATATGGTAGA 17
               ||||||||||||
Db          21 TGATATGGTAGA 10
```

RESULT 12
US-09-396-196G-94665/c
; Sequence 94665, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94665
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-94665

Query Match 41.4%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           6 TGATATGGTAGA 17
               ||||||||||||
Db          19 TGATATGGTAGA 8
```

RESULT 13
US-09-513-999C-22225
; Sequence 22225, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 22225
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-22225

Query Match 41.4%; Score 12; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           5 GTGATATGGTAG 16
               ||||||||||||
Db          20 GTGATATGGTAG 31
```

RESULT 14
US-09-021-701-1077/c
; Sequence 1077, Application US/09021701
; Patent No. 6251588
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.

```
;    APPLICANT:  Kincaid, Robert H.
;    TITLE OF INVENTION:  Methods for evaluating oligonucleotide
;    TITLE OF INVENTION:  probe sequences
;    NUMBER OF SEQUENCES:  1165
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Records Manager, Legal Department, Hewlett-Packard Company M/S 20
;      STREET:  3000 Hanover Street
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/021,701
;      FILING DATE:  10-FEB-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Choi, Wendy A.
;      REGISTRATION NUMBER:  36,697
;      REFERENCE/DOCKET NUMBER:  10971464-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-236-2386
;      TELEFAX:  650-852-8063
;  INFORMATION FOR SEQ ID NO:  1077:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-021-701-1077

  Query Match             37.9%;  Score 11;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 TAGATACAGGA 24
               ||||||||||| 
Db          20 TAGATACAGGA 10


RESULT 15
US-09-021-701-1078/c
; Sequence 1078, Application US/09021701
; Patent No. 6251588
;  GENERAL INFORMATION:
;    APPLICANT:  Shannon, Karen W.
;    APPLICANT:  Wolber, Paul K.
;    APPLICANT:  Delenstarr, Glenda C.
;    APPLICANT:  Webb, Peter G.
;    APPLICANT:  Kincaid, Robert H.
;    TITLE OF INVENTION:  Methods for evaluating oligonucleotide
;    TITLE OF INVENTION:  probe sequences
;    NUMBER OF SEQUENCES:  1165
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Records Manager, Legal Department, Hewlett-Packard Company M/S 20
;      STREET:  3000 Hanover Street
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/021,701
;      FILING DATE:  10-FEB-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Choi, Wendy A.
;      REGISTRATION NUMBER:  36,697
;      REFERENCE/DOCKET NUMBER:  10971464-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-236-2386
;      TELEFAX:  650-852-8063
;  INFORMATION FOR SEQ ID NO:  1078:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-021-701-1078

  Query Match             37.9%;  Score 11;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 TAGATACAGGA 24
               ||||||||||| 
Db          19 TAGATACAGGA 9


Search completed: March  5, 2006, 19:10:48
Job time : 79 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 19:08:04 ; Search time 78 Seconds
(without alignments)
660.888 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word-size : 1

Total number of hits satisfying chosen parameters: 1426356

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12	41.4	19	3	US-09-696-791-3968	Sequence 3968, Ap
	2	12	41.4	19	3	US-09-696-791-3969	Sequence 3969, Ap
	3	12	41.4	19	3	US-09-696-791-3970	Sequence 3970, Ap
	4	12	41.4	25	3	US-09-396-196G-22482	Sequence 22482, A
c	5	12	41.4	25	3	US-09-396-196G-59285	Sequence 59285, A
c	6	12	41.4	25	3	US-09-396-196G-79525	Sequence 79525, A
	7	11	37.9	18	2	US-08-190-199A-33	Sequence 33, Appl
	8	11	37.9	19	3	US-09-422-978-4722	Sequence 4722, Ap
c	9	11	37.9	20	2	US-07-922-723A-6	Sequence 6, Appli
c	10	11	37.9	20	2	US-07-799-828C-6	Sequence 6, Appli
c	11	11	37.9	20	2	US-08-074-275-6	Sequence 6, Appli
c	12	11	37.9	20	2	US-08-480-366-6	Sequence 6, Appli
c	13	11	37.9	20	2	US-07-952-277A-6	Sequence 6, Appli
c	14	11	37.9	20	3	US-09-283-040-8	Sequence 8, Appli
c	15	11	37.9	20	3	US-09-413-304-9	Sequence 9, Appli
	16	11	37.9	20	3	US-09-659-791A-76	Sequence 76, Appl
c	17	11	37.9	20	3	US-09-817-856-9	Sequence 9, Appli
	18	11	37.9	20	3	US-09-780-175-144	Sequence 144, App
c	19	11	37.9	23	3	US-09-167-681-19	Sequence 19, Appl
	20	11	37.9	23	3	US-10-164-230-17	Sequence 17, Appl
c	21	11	37.9	25	3	US-09-396-196G-8219	Sequence 8219, Ap
c	22	11	37.9	25	3	US-09-396-196G-20870	Sequence 20870, A
c	23	11	37.9	25	3	US-09-396-196G-20872	Sequence 20872, A
c	24	11	37.9	25	3	US-09-396-196G-42248	Sequence 42248, A
c	25	11	37.9	25	3	US-09-396-196G-84796	Sequence 84796, A
c	26	11	37.9	25	3	US-09-396-196G-84797	Sequence 84797, A
c	27	11	37.9	25	3	US-09-396-196G-84813	Sequence 84813, A
c	28	11	37.9	25	3	US-09-396-196G-84814	Sequence 84814, A
c	29	11	37.9	25	3	US-09-396-196G-87409	Sequence 87409, A
c	30	11	37.9	25	3	US-09-396-196G-87420	Sequence 87420, A
c	31	11	37.9	25	3	US-09-396-196G-87421	Sequence 87421, A
c	32	11	37.9	25	3	US-09-396-196G-87422	Sequence 87422, A
c	33	11	37.9	25	3	US-09-396-196G-95386	Sequence 95386, A
c	34	11	37.9	25	3	US-09-396-196G-118491	Sequence 118491,
c	35	11	37.9	25	3	US-09-396-196G-118492	Sequence 118492,
	36	11	37.9	39	3	US-09-452-638-46	Sequence 46, Appl
c	37	11	37.9	43	3	US-09-641-638-780	Sequence 780, App
c	38	11	37.9	43	3	US-10-170-097-780	Sequence 780, App
c	39	11	37.9	44	3	US-09-354-409-3	Sequence 3, Appli
	40	11	37.9	45	2	US-08-853-217-22	Sequence 22, Appl
	41	11	37.9	46	2	US-08-495-695B-14	Sequence 14, Appl
	42	11	37.9	46	3	US-09-430-775-14	Sequence 14, Appl
	43	11	37.9	46	6	PCT-US94-14436-14	Sequence 14, Appl
	44	11	37.9	47	3	US-09-422-978-2911	Sequence 2911, Ap
	45	11	37.9	54	2	US-08-311-486C-1123	Sequence 1123, Ap

ALIGNMENTS

RESULT 1
US-09-696-791-3968
; Sequence 3968, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3968
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3968

Query Match 41.4%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTACCATAGAG 21
||||||||||||
Db 8 GTTACCATAGAG 19

RESULT 2
US-09-696-791-3969
; Sequence 3969, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: SKIN AND EYE DISEASES
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3969
; LENGTH: 19

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3969

  Query Match             41.4%;  Score 12;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
               ||||||||||||
Db          7 GTTACCATAGAG 18


RESULT 3
US-09-696-791-3970
; Sequence 3970, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 3970
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: PCNA HH ribozyme binding site
US-09-696-791-3970

  Query Match             41.4%;  Score 12;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 9.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
               ||||||||||||
Db          2 GTTACCATAGAG 13


RESULT 4
US-09-396-196G-22482
; Sequence 22482, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22482
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-22482

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.7e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GTCAGAGGTTAC 14
               ||||||||||||
Db         14 GTCAGAGGTTAC 25


RESULT 5
US-09-396-196G-59285/c
; Sequence 59285, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59285
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-59285

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.7e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 ACCATAGAGCCA 24
               ||||||||||||
Db         14 ACCATAGAGCCA 3


RESULT 6
US-09-396-196G-79525/c
; Sequence 79525, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79525
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-79525

  Query Match             41.4%;  Score 12;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 9.7e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
               ||||||||||||
Db         23 GTTACCATAGAG 12


RESULT 7
US-08-190-199A-33
; Sequence 33, Application US/08190199A
; Patent No. 5830663
```

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;  GENERAL INFORMATION:
;    APPLICANT:  EMBLETON, Michael J.
;    APPLICANT:  GOROCHOV, Guy
;    APPLICANT:  JONES, Peter T.
;    APPLICANT:  WINTER, Gregory P.
;    TITLE OF INVENTION:  TREATMENT OF CELL POPULATIONS
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,199A
;      FILING DATE:  13-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/01483
;      FILING DATE:  10-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9212419.7
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9117352.6
;      FILING DATE:  10-AUG-1991
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-190-199A-33

  Query Match             37.9%;  Score 11;  DB 2;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGC 22
              ||||||||||
Db          4 TACCATAGAGC 14


RESULT 8
US-09-422-978-4722
; Sequence 4722, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4722
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-17343 for SEQ 788,
US-09-422-978-4722

  Query Match             37.9%;  Score 11;  DB 3;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GGTTACCATAG 19
              ||||||||||
Db          9 GGTTACCATAG 19


RESULT 9
US-07-922-723A-6/c
; Sequence 6, Application US/07922723A
; Patent No. 5369004
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Mihael H. Polymeropoulos
;    APPLICANT:  and Carl R. Merril
;    TITLE OF INVENTION:  FIVE HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  REPEAT POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/922,723A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34506
;      REFERENCE/DOCKET NUMBER:  717081B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-922-723A-6

  Query Match             37.9%;  Score 11;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8


RESULT 10
US-07-799-828C-6/c
; Sequence 6, Application US/07799828C
; Patent No. 5378602
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Carl R. Merril and
```

```
;    APPLICANT:  Mihael H. Polymeropoulos
;    TITLE OF INVENTION:  TWENTY SEVEN HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  MICROSATELLITE REPEAT
;    TITLE OF INVENTION:  POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/799,828C
;      FILING DATE:  19911127
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34,506
;      REFERENCE/DOCKET NUMBER:  717081A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-799-828C-6

  Query Match             37.9%;  Score 11;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8


RESULT 11
US-08-074-275-6/c
; Sequence 6, Application US/08074275
; Patent No. 5468610
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Carl R. Merril and
;    APPLICANT:  Mihael H. Polymeropoulos
;    TITLE OF INVENTION:  THREE HIGHLY INFORMATIVE REPEAT
;    TITLE OF INVENTION:  POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/074,275
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/707,501
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  J.G. Mullins
;      REGISTRATION NUMBER:  33073
;      REFERENCE/DOCKET NUMBER:  717081
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-074-275-6

  Query Match             37.9%;  Score 11;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8


RESULT 12
US-08-480-366-6/c
; Sequence 6, Application US/08480366
; Patent No. 5721100
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Carl R. Merril and
;    APPLICANT:  Mihael H. Polymeropoulos
;    TITLE OF INVENTION:  THREE HIGHLY INFORMATIVE REPEAT
;    TITLE OF INVENTION:  POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,366
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  J.G. Mullins
;      REGISTRATION NUMBER:  33073
;      REFERENCE/DOCKET NUMBER:  717081
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-480-366-6

  Query Match             37.9%;  Score 11;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8
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RESULT 13
US-07-952-277A-6/c
; Sequence 6, Application US/07952277A
; Patent No. 5861504
; GENERAL INFORMATION:
;    APPLICANT:  Drs. Mihael H. Polymeropoulos
;    APPLICANT:  and Carl R. Merril
;    TITLE OF INVENTION:  ELEVEN HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  REPEAT POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/952,277A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34506
;      REFERENCE/DOCKET NUMBER:  717081C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-952-277A-6

  Query Match             37.9%;  Score 11;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8


RESULT 14
US-09-283-040-8/c
; Sequence 8, Application US/09283040
; Patent No. 6162604
; GENERAL INFORMATION:
;  APPLICANT: Jacob, C.
;  TITLE OF INVENTION: METHODS FOR DETERMINING GENETIC
;  TITLE OF INVENTION: PREDISPOSITION TO SYSTEMIC LUPUS ERYTHEMATOSUS AND OTHER
;  TITLE OF INVENTION: AUTOIMMUNE DISEASES BY GENOTYPING IL-10, BCL-2, FAS-L, AND
;  TITLE OF INVENTION: OTHER APOPTOTIC GENES.
;  FILE REFERENCE: IMSCI.010A
;  CURRENT APPLICATION NUMBER: US/09/283,040
;  CURRENT FILING DATE: 1999-04-01
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR primer to CTLA-4 microsatellite.
;  PUBLICATION INFORMATION:
;   AUTHORS: Polymeropoules, et al.
;   JOURNAL: Nucleic Acids Research
;   VOLUME: 19
;   ISSUE: 1991
;   PAGES: 4018
US-09-283-040-8

  Query Match             37.9%;  Score 11;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCAC 25
              ||||||||||
Db         18 CATAGAGCCAC 8


RESULT 15
US-09-413-304-9/c
; Sequence 9, Application US/09413304
; Patent No. 6207387
; GENERAL INFORMATION:
;  APPLICANT: Louis J. Elsas II
;  APPLICANT: K. Muralidharan
;  TITLE OF INVENTION: MOLECULAR DIAGNOSTICS FOR GALACTOSEMIA
;  FILE REFERENCE: 05010.0079
;  CURRENT APPLICATION NUMBER: US/09/413,304
;  CURRENT FILING DATE: 1999-10-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. 6207387e =
US-09-413-304-9

  Query Match             37.9%;  Score 11;  DB 3;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 TAGAGCCACTA 27
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Db         13 TAGAGCCACTA 3


Search completed: March  5, 2006, 19:10:48
Job time : 78 secs
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 22:20:14 ; Search time 2987.5 Seconds
(without alignments)
454.167 Million cell updates/sec

Title: US-10-720-424B-8
Perfect score: 29
Sequence: 1 gcgtcagaggttaccatagagccactagg 29

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word-size : 1

Total number of hits satisfying chosen parameters: 777740

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	13	44.8	75	10	BX891062	BX891062 Arabidops
	2	13	44.8	78	9	AZ422866	AZ422866 1M0201C08
c	3	13	44.8	91	11	CR359087	CR359087 Arabidops
	4	13	44.8	96	9	B07639	B07639 CDC1e4 Cri
c	5	12	41.4	44	9	AZ801332	AZ801332 2M0059E17
c	6	12	41.4	69	10	BX288836	BX288836 Arabidops
c	7	12	41.4	71	10	AL768653	AL768653 Arabidops
	8	12	41.4	75	7	CK589249	CK589249 IST_WI5_4
c	9	12	41.4	76	6	CF800008	CF800008 RpL3i-II-
c	10	12	41.4	76	10	CZ259321	CZ259321 CC0712 Sa
c	11	12	41.4	80	9	BH221305	BH221305 1006100E1
c	12	12	41.4	80	10	AL947277	AL947277 Arabidops
c	13	12	41.4	81	5	BU101523	BU101523 PRODG1GID
c	14	12	41.4	83	9	AZ830956	AZ830956 2M0110P22
	15	12	41.4	83	10	AJ595832	AJ595832 Arabidops
	16	12	41.4	89	9	BH860887	BH860887 Gm_SIUb00
	17	12	41.4	90	1	AA832122	AA832122 oc97h09.s
	18	12	41.4	91	1	AV563280	AV563280 AV563280
	19	12	41.4	93	10	CG529767	CG529767 OST110652
c	20	12	41.4	95	10	BX896965	BX896965 Arabidops
c	21	12	41.4	96	5	BU873739	BU873739 Q059D03 P
c	22	12	41.4	97	10	AL942821	AL942821 Arabidops
c	23	12	41.4	98	5	BU831039	BU831039 T016D07 P
c	24	12	41.4	99	6	CD954464	CD954464 SBO_322 G
c	25	12	41.4	99	8	W08501	W08501 mb47d12.r1
	26	12	41.4	100	1	AI040719	AI040719 ox26b10.s
	27	12	41.4	100	7	CK895114	CK895114 SGP154364
	28	12	41.4	100	7	CK896099	CK896099 SGP158635
	29	11	37.9	49	1	AA234629	AA234629 zr75b05.r
	30	11	37.9	50	10	CW020438	CW020438 GC0700 TI
c	31	11	37.9	50	11	CR217452	CR217452 Reverse s
c	32	11	37.9	51	9	BZ382023	BZ382023 SALK_1177
	33	11	37.9	51	10	CW083054	CW083054 104_425_1
c	34	11	37.9	53	6	CF660841	CF660841 CcLM09a32
c	35	11	37.9	56	9	AZ807027	AZ807027 2M0069A03
c	36	11	37.9	60	1	AJ654040	AJ654040 AJ654040
c	37	11	37.9	62	10	BX530887	BX530887 Arabidops
	38	11	37.9	63	7	CK814651	CK814651 Rasgsc531
c	39	11	37.9	63	9	AZ609630	AZ609630 1M0434E04
	40	11	37.9	66	10	BX205284	BX205284 Danio rer
c	41	11	37.9	67	5	BX553131	BX553131 BX553131
c	42	11	37.9	67	10	AL751479	AL751479 Arabidops
	43	11	37.9	67	10	CG532847	CG532847 OST117308
	44	11	37.9	68	10	BX572204	BX572204 Arabidops
c	45	11	37.9	69	10	BX536465	BX536465 Arabidops

ALIGNMENTS

RESULT 1
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LOCUS BX891062 75 bp DNA linear GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-445F03-023515, genomic survey sequence.
ACCESSION BX891062
VERSION BX891062.1 GI:39923557
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 75)
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g44170. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .75
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-445F03-023515"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN

Query Match 44.8%; Score 13; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAGGTTACCATAG 19
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Db 64 GAGGTTACCATAG 52

RESULT 2
AZ422866
LOCUS AZ422866 78 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0201C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0201C08 R, genomic survey sequence.
ACCESSION AZ422866
VERSION AZ422866.1 GI:10546795
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 78)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: C column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 78.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0201C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 44.8%; Score 13; DB 9; Length 78;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGGTTACCATAGA 20
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Db 42 AGGTTACCATAGA 54

RESULT 3
CR359087/c
LOCUS CR359087 91 bp DNA linear GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-733D10-025420, genomic survey sequence.
ACCESSION CR359087
VERSION CR359087.1 GI:45542009
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 91)
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g36870. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

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FEATURES             Location/Qualifiers
     source          1. .91
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                     /mol_type="genomic DNA"
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                     /clone="GK-733D10-025420"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pGABI1 (GenBank accession number: AY529716). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match           44.8%;  Score 13;  DB 11;  Length 91;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TACCATAGAGCCA 24
              |||||||||||||
Db         54 TACCATAGAGCCA 42


RESULT 4
B07639
LOCUS       B07639                    96 bp    DNA     linear   GSS 17-JAN-1998
DEFINITION  CDC1e4 Cri du chat, exon trapped products Homo sapiens genomic
            clone CDC1e4, genomic survey sequence.
ACCESSION   B07639
VERSION     B07639.1  GI:2781465
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 96)
  AUTHORS   Church,D.M., Yang,J., Shiang,R., Wasmuth and J.J.
  TITLE     A High Resolution Physical and Transcription map for the Cri du
            chat region of human chromosome 5p
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Rita Shiang
            Shiang lab
            University of California- Irvine
            240D Med. Sci. I, UCI-COM, Irvine, CA 92697-1700, USA
            Tel: (714)824-6792
            Fax: (714)824-3403
            Email: rshiang@chrom5.hsis.uci.edu
            Insert Length: 96   Std Error: 0.00
            Class: exon-trapped.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="CDC1e4"
                     /clone_lib="Cri du chat, exon trapped products"
                     /note="Exon trapped products from the CDC critical region
                     associated with mental retardation and facial
                     dysmorphism."
ORIGIN

  Query Match           44.8%;  Score 13;  DB 9;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GAGGTTACCATAG 19
              |||||||||||||
Db         72 GAGGTTACCATAG 84


RESULT 5
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LOCUS       AZ801332                  44 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0059E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0059E17 R, genomic survey sequence.
ACCESSION   AZ801332
VERSION     AZ801332.1  GI:12953655
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 44)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0059  row: E  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 44.
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0059E17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           41.4%;  Score 12;  DB 9;  Length 44;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          13 ACCATAGAGCCA 24
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Db          24 ACCATAGAGCCA 13


RESULT 6
BX288836/c
LOCUS       BX288836                69 bp    DNA     linear   GSS 02-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-420D05-018101,
            genomic survey sequence.
ACCESSION   BX288836
VERSION     BX288836.1  GI:28887832
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4  (bases 1 to 69)
  AUTHORS   Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At1g48700.
            Details on the protocols used for generation of the sequence are
            described in References 1-3. The sequences are generated at the MPI
            for Plant Breeding Research in the context of the GABI-Kat project.
            GABI-Kat is part of the German Plant Genomics program designated
            'GABI'. Information on line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .69
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                     /mol_type="genomic DNA"
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                     /clone="GK-420D05-018101"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 10;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          14 CCATAGAGCCAC 25
               ||||||||||||
Db          64 CCATAGAGCCAC 53


RESULT 7
AL768653/c
LOCUS       AL768653                71 bp    DNA     linear   GSS 01-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-076E01-011920,
            genomic survey sequence.
ACCESSION   AL768653
VERSION     AL768653.1  GI:21521772
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4  (bases 1 to 71)
  AUTHORS   Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion within the locus defined by BAC clone
            MRC8. Details on the protocols used for generation of the sequence
            are described in References 1-3. The sequences are generated at the
            MPI for Plant Breeding Research in the context of the GABI-Kat
            project. GABI-Kat is part of the German Plant Genomics program
            designated 'GABI'. Information on line availability can be found
            at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .71
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3702"
                     /clone="GK-076E01-011920"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 10;  Length 71;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          14 CCATAGAGCCAC 25
               ||||||||||||
Db          55 CCATAGAGCCAC 44


RESULT 8
CK589249
LOCUS       CK589249                 75 bp    mRNA    linear   EST 16-JAN-2004
DEFINITION  IST_WI5_41889 AD-ORFeome1.0 library Caenorhabditis elegans cDNA 5'
            similar to F09F7.5, mRNA sequence.
ACCESSION   CK589249
VERSION     CK589249.1  GI:40973178
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Li,S., Armstrong,C.M., Bertin,N., Ge,H., Milstein,S., Boxem,M.,
            Vidalain,P.O., Han,J.D., Chesneau,A., Hao,T., Goldberg,D.S., Li,N.,
            Martinez,M., Rual,J.F., Lamesch,P., Xu,L., Tewari,M., Wong,S.L.,
            Zhang,L.V., Berriz,G.F., Jacotot,L., Vaglio,P., Reboul,J.,
            Hirozane-Kishikawa,T., Li,Q., Gabel,H.W., Elewa,A., Baumgartner,B.,
            Rose,D.J., Yu,H., Bosak,S., Sequerra,R., Fraser,A., Mango,S.E.,
            Saxton,W.M., Strome,S., Van Den Heuvel,S., Piano,F.,
            Vandenhaute,J., Sardet,C., Gerstein,M., Doucette-Stamm,L.,
            Gunsalus,K.C., Harper,J.W., Cusick,M.E., Roth,F.P., Hill,D.E. and
            Vidal,M.
  TITLE     A Map of the Interactome Network of the Metazoan C. elegans
  JOURNAL   Science (2004) In press
COMMENT     Contact: Vidal M
            Marc Vidal Laboratory
            Dana Farber Cancer Institute
            1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
            Tel: 617 632 5180
            Fax: 617 632 5739
            Email: Marc_Vidal@dfci.harvard.edu
            For the purpose of protein interaction mapping, we generated a C.
            elegans a normalized library of ORF fused to the AD-encoding
            sequence of the yeast transcription factor GAL4. Those ORFs derive
            from the PCR amplification between the predicted (WS9) initiation
            and termination codons, using the cDNA library AD-wrmcDNA as
            template This Interacting Sequence Tag IST_WI5_41889 (F09F7.5)
            interacts as a prey with the bait W09H1.6
            PCR PRimers
            FORWARD: CGCGTTTGGAATCACTACAGGG
            BACKWARD: GGAGACTTGACCAAACCTCTGGCG
            Insert Length: 75   Std Error: 74.00
            Plate: 547  row: 08  column: H
            Seq primer: CGCGTTTGGAATCACTACAGGG
            High quality sequence stop: 74
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="Caenorhabditis elegans"
                     /mol_type="mRNA"
                     /strain="N2"
                     /db_xref="taxon:6239"
                     /sex="male, hermaphrodite"
                     /dev_stage="embryos, L1, L2, L3, L4, adult, dauer"
                     /clone_lib="AD-ORFeome1.0 library"
                     /note="Vector: pDestPC86/Cyh; For the purpose of protein
                     interaction mapping, predicted protein-encoding ORFs were
                     amplified by PCR precisely between the predicted (WS9
                     version of WormPep) initiation and termination codons,
                     using a cDNA library (AD-wrmcDNA library - Walhout etal.
                     Methods Enzymol. 2000;328:575-92) as template. The
                     resulting 11,984 Gateway cloned ORFs along with the
                     attempted ones were transfered into a two-hybrid
                     Destination vector downstream of the vector sequence
                     encoding the activation domain (AD) of the yeast GAL4
                     transcription factor. Those constructs were pooled
                     together to constitute a 'normalized' AD-ORFeome1.1
                     library. Reference - Reboul J, Vaglio P etal C. elegans
                     ORFeome version 1.1: experimental verification of the
                     genome annotation and resource for proteome-scale protein
                     expression. Nat Genet. 2003 May;34(1):35-41. PMID:
                     12679813)"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 7;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           3 GTCAGAGGTTAC 14
               ||||||||||||
Db          40 GTCAGAGGTTAC 51


RESULT 9
CF800008/c
LOCUS       CF800008                 76 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  RpL3i-II-B7 RpL3i Rhopalosiphum padi cDNA clone RpL3iII7B 5', mRNA
            sequence.
ACCESSION   CF800008
VERSION     CF800008.1  GI:37804578
KEYWORDS    EST.
SOURCE      Rhopalosiphum padi (bird cherry-oat aphid)
  ORGANISM  Rhopalosiphum padi
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Aphidini; Rhopalosiphum.
REFERENCE   1  (bases 1 to 76)
  AUTHORS   Tagu,C., Prunier-Leterme,N., Legeai,F., Gauthier,J.P., Duclert,A.,
            Sabater-Munoz,B., Bonhomme,J. and Simon,J.C.
  TITLE     Annotated expressed sequence tags for studies of the regulation of
            reproductive modes in aphids
  JOURNAL   Insect. Biochem. Mol. Biol. 34 (8), 809-822 (2004)
   PUBMED   15262285
COMMENT     Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            PCR PRimers
            FORWARD: GCCGCATAACTTCGTATAGCA
            Plate: II  row: B  column: 7.
FEATURES             Location/Qualifiers
     source          1. .76
                     /organism="Rhopalosiphum padi"
                     /mol_type="mRNA"
                     /strain="h3"
                     /db_xref="taxon:40932"
                     /clone="RpL3iII7B"
                     /tissue_type="whole insect"
                     /dev_stage="third instar nymph (L3)"
                     /lab_host="TOP10"
                     /clone_lib="RpL3i"
                     /note="Vector: pDNR-LIB; Site_1: SfiIA; Site_2: SfiIB;
                     aphids inoculated on one-week old wheat germinations in
                     test tube under non sterile conditions. experimental
                     condition: short photoperiod (10-hr light/14-hr dark at
                     12oC during 12 days)"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 6;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 ACCATAGAGCCA 24
               ||||||||||||
Db          72 ACCATAGAGCCA 61


RESULT 10
CZ259321/c
```

```
LOCUS       CZ259321                 76 bp    mRNA    linear   GSS 11-APR-2005
DEFINITION  CC0712 Sanger Institute Gene Trap Library pGT0lxfT2 Mus musculus
            cDNA, mRNA sequence.
ACCESSION   CZ259321
VERSION     CZ259321.1  GI:60282982
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 76)
  AUTHORS   Sanger Intitute Gene Trap Resource - SIGTR.
  TITLE     http://www.sanger.ac.uk/PostGenomics/genetrap/
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Sanger Institute Gene Trap Resource - SIGTR
            Wellcome Trust Sanger Institute
            Email: info.genetrap@sanger.ac.uk
            Sequence tag generated by 5' RACE of total RNA from gene trap ES
            cell line. ES cell lines harboring insertion mutation of target
            gene are available upon request from Sanger Institute Gene Trap
            Resource. Annotation information available from
            http://www.sanger.ac.uk/PostGenomics/genetrap/
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .76
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129 OLA"
                     /db_xref="taxon:10090"
                     /sex="Male"
                     /cell_type="Embryonic Stem Cell"
                     /clone_lib="Sanger Institute Gene Trap Library pGT0lxfT2"
                     /note="Vector: pGT0lxfT2"
ORIGIN

  Query Match             41.4%;  Score 12;  DB 10;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 CATAGAGCCACT 26
              ||||||||||||
Db         50 CATAGAGCCACT 39


RESULT 11
BH221305/c
LOCUS       BH221305                 80 bp    DNA     linear   GSS 08-NOV-2001
DEFINITION  1006100E11.y1 1006 - RescueMu Grid G Zea mays genomic, genomic
            survey sequence.
ACCESSION   BH221305
VERSION     BH221305.1  GI:16815564
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 80)
  AUTHORS   Walbot,V.
  TITLE     Maize genomic sequences found using engineered RescueMu transposon
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 1006100  row: 31
            Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source          1. .80
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /cultivar="mixed background W23/A188/B73"
                     /db_xref="taxon:4577"
                     /tissue_type="leaf"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="1006 - RescueMu Grid G"
                     /note="Organ: leaf; Vector: RescueMu (engineered from
                     pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
                     RescueMu is a 4.9 kb, modified maize Mu transposon
                     designed to allow plasmid rescue from total genomic DNA.
                     Mu elements insert preferentially into transcription
                     units. For more information on RescueMu, go to the web
                     site 'www.zmdb.iastate.edu' and follow the links for
                     'RescueMu.' Grid G was grown at Stanford in 2000. DNA was
                     extracted from leaf punches, double digested using BamHI
                     and BglII, and ligated to form circular plasmids. DH10B
                     cells were transformed and then screened on LB plates with
                     ampicillin."
ORIGIN

  Query Match             41.4%;  Score 12;  DB 9;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTACCATAGAG 21
              ||||||||||||
Db         32 GTTACCATAGAG 21


RESULT 12
AL947277/c
LOCUS       AL947277                 80 bp    DNA     linear   GSS 02-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-303A11-015563,
            genomic survey sequence.
ACCESSION   AL947277
VERSION     AL947277.1  GI:24403899
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4  (bases 1 to 80)
  AUTHORS   Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At3g19680.
            Details on the protocols used for generation of the sequence are
```

described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES Location/Qualifiers
source 1. .80
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-303A11-015563"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 41.4%; Score 12; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTACCATAGAG 21
||||||||||||
Db 42 GTTACCATAGAG 31

RESULT 13
BU101523/c
LOCUS BU101523 81 bp mRNA linear EST 25-MAR-2004
DEFINITION PRODG1GID25R1 Compugen_targeted_mRNA_sequencing Homo sapiens cDNA, mRNA sequence.
ACCESSION BU101523
VERSION BU101523.1 GI:45736923
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 81)
AUTHORS Xie,H., Diber,A., Pollack,S., Nemzer,S., Safer,H., Meloon,B., Olson,A., Hwang,J.-J., Endress,G.A., Savitsky,K. and Gill-More,R.
TITLE Bridging expressed sequence alignments through targeted cDNA sequencing
JOURNAL Genomics 83 (4), 572-576 (2004)
PUBMED 15028280
COMMENT Contact: Xie H
Compugen
7 Center Drive, Suite 9, Jamesburg, NJ 08831, USA
Tel: 609-655-5105 X 26
Fax: 609-655-5114
Email: han@cgen.com.

FEATURES Location/Qualifiers
source 1. .81
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Compugen_targeted_mRNA_sequencing"
/note="These sequences resulted from single pass sequencing of PCR products from Compugen targeted mRNA sequencing project. PCR primers and nested primers were designed to join two neighboring expressed sequence contigs based on Compugen LEADS expressed sequence cluster and assembly platform. Reverse transcriptase PCR and nested PCR reactions were performed by Protedyne Inc. (Windsor, CT 06095, USA) on normal human heart, brain, lung, liver, placenta, and testis poly mRNA preparations from Origen (Rockville, MD 20850, USA) with reagents from Invitrogen (Carlsbad, California 92008). PCR products were sequenced by Qiagen (Valencia, CA 91355)."

ORIGIN

Query Match 41.4%; Score 12; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 TACCATAGAGCC 23
||||||||||||
Db 39 TACCATAGAGCC 28

RESULT 14
AZ830956/c
LOCUS AZ830956 83 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0110P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0110P22 F, genomic survey sequence.
ACCESSION AZ830956
VERSION AZ830956.1 GI:13000864
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 83)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: P column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 83.

FEATURES Location/Qualifiers
source 1. .83
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0110P22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN

Query Match 41.4%; Score 12; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGGTTACCATAG 19
||||||||||||
Db 81 AGGTTACCATAG 70

RESULT 15
AJ595832
LOCUS AJ595832 83 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
424E08, genomic survey sequence.
ACCESSION AJ595832
VERSION AJ595832.1 GI:37945460
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED 12446565
REFERENCE 2 (bases 1 to 83)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .83
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="424E08"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature 1. .83
/note="T-DNA flanking sequence
left border"
ORIGIN

Query Match 41.4%; Score 12; DB 10; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 ACCATAGAGCCA 24
||||||||||||
Db 64 ACCATAGAGCCA 75

Search completed: March 6, 2006, 00:16:52
Job time : 2990.5 secs